

## **FIGURE 1**

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGTATG  
AGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAACAGAAAACCTGTTAGAAATGTGGTGGT  
TTCAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCTTTTCATATTT  
TCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGG  
TACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGGCAGTTTTATGCATTG  
CTACCATTTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAAGAGAACGTTATCATCAA  
TTAAACAAGGCTGGCCTTGACTTGGAATACTGAGTTGTTTAGGACTTTCTATTGTGGCAAACCT  
CCAGAAAACAACCCTTTTTGGCTGCACATGTAAGTGGAGCTGTGCTTACCTTTGGTATGGGCTCAT  
TATATATGTTTGTTCAGACCATCCTTTCCTACCAAATGCAGCCCAAATCCATGGCAAACAAGTC  
TTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGGAGTAAGTGCACCTTAGCATGCTGACTTGCTC  
ATCAGTTTTGCACAGTGGCAATTTTGGGACTGATTTAGAACAGAACTCCATTGGAACCCCGAGG  
ACAAAGGTTATGTGCTTCACATGATCACTACTGCAGCAGAATGGTCTATGTCATTTTCCTTCTTT  
GGTTTTTTCCTGACTTACATTCGTGATTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACA  
TGGATTAACCTCTATGACACTGCACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCCA  
GAGATATTTGATGAAAGGATAAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGG  
TTCACAGAAGTTGCTTATTTCTTCTCTGAAATTTTCAACCACTTAATCAAGGCTGACAGTAACACT  
GATGAATGCTGATAATCAGGAAACATGAAAGAAGCCATTTGATAGATTATTCTAAAGGATATCAT  
CAAGAAGACTATTAAAAACACCTATGCCTATACTTTTTTATCTCAGAAAATAAAGTCAAAAGACT  
ATG

## **FIGURE 2**

<subunit 1 of 1, 266 aa, 1 stop

<MW: 29766, pI: 8.39, NX(S/T): 0

MWWFQQGLSFLPSALVIWTSAAFIIFSYYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNIAAV  
LCIATIIYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSGAVLTFG  
MGSLYMFVQTIILSYQMOPKIHGKQVFWIRLLLVIWCGVSALSMLTCSSVLHSGNFGTDLEQKLHW  
NPEDKGYVLHMITTAAEWSMSFSFFGFFLTYYIRDFQKISLRVEANLHGLTLYDTAPCPINNERTR  
LLSRDI

### **Important features:**

#### **Type II transmembrane domain:**

amino acids 13-33

#### **Other Transmembrane domains:**

amino acids 54-73, 94-113, 160-180, 122-141

#### **N-myristoylation sites.**

amino acids 57-63, 95-101, 99-105, 124-130, 183-189

### FIGURE 3

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGCGAGTCCCGGCTGCAGCACCTGGGAGAAGGCAGACC  
GTGTGAGGGGGCCTGTGGCCCCAGCGTGTGTGGCCTCGGGGAGTGGGAAGTGGAGGCAGGAGCCCTTC  
CTTACACTTCGCCCATGAGTTTCTCATCGACTCCAGCATCATGATTACCTCCCAGATACTATTTTTTG  
GATTTGGGTGGCTTTTCTTCATGCGCCAATTGTTAAAGACTATGAGATACGTAGTATGTTGTACAG  
GTGATCTTCTCCGTGACGTTTGCATTTTCTTGCAACCATGTTTGAGCTCATCATCTTTGAAATCTTAGG  
AGTATTGAATAGCAGCTCCCCTTATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGG  
TTTTTCATGGTGCCTTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCATAAACAACGA  
CTGCTTTTTTCTGTCCTTATGGCTGACCTTTATGTATTTCTTCTGGAACTAGGAGATCCCTTTCC  
CATTCTCAGCCCAAACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTGGTGTGATTGGAG  
TGACTCTCATGGCTCTTCTTTCTGGATTGGTGTGTCAACTGCCCATACACTTACATGTCTTACTTC  
CTCAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATATGAT  
CATAAGCAAAAAGAAAAGGATGGCAATGGCAGGAGAACAATGTTCCAGAAGGGGGAAGTGCATAACA  
AACCATCAGGTTTTCTGGGAATGATAAAAAGTGTACCACCTCAGCATCAGGAAGTGAAAACTTACT  
CTTATTCAACAGGAAGTGGATGCTTTGGAAGAATTAAGCAGGCAGCTTTTTCTGGAAACAGCTGATCT  
ATATGCTACCAAGGAGAGAATAGAATACTCCAAAACCTTCAAGGGGAAATATTTTAATTTTCTTGGTT  
ACTTTTTCTCTATTTACTGTGTTTGGAAAATTTTCATGGCTACCATCAATATTGTTTTTGATCGAGTT  
GGGAAAACGGATCCTGTACAAAGAGGCATTGAGATCACTGTGAATTATCTGGGAATCCAATTTGATGT  
GAAGTTTTGGTCCCAACACATTTCCCTTCATTCTTGTGGAATAATCATCGTCACATCCATCAGAGGAT  
TGCTGATCACTCTTACCAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCCTCCAATGTCTTGTCTG  
CTATTAGCACAGATAATGGGCATGTACTTGTCTCCTCTGTGCTGCTGATCCGAATGAGTATGCCTTT  
AGAATACCGCACCATAATCACTGAAGTCCTTGGAGAACTGCAGTTCAACTTCTATCACCCTTGGTTTG  
ATGTGATCTTCCCTGGTCAGCGCTCTCTCTAGCATACTCTTCTCTATTTGGCTCACAAACAGGCACCA  
GAGAAGCAAATGGCACCTTGAACTTAAGCCTACTACAGACTGTTAGAGGCCAGTGGTTTCAAATTTA  
GATATAAGAGGGGGGAAAAATGGAACAGGGCCTGACATTTTATAAACAAACAAAATGCTATGGTAGC  
ATTTTTACCTTCATAGCATACTCCTTCCCCGTGAGGTGATACTATGACCATGAGTAGCATCAGCCAG  
AACATGAGAGGGGAGAACTAATCAAGACAATACTCAGCAGAGAGCATCCCGTGTGGATATGAGGCTGG  
TGTAAGGCGGAGAGGAGCCAAGAACTAAAGGTGAAAAATACACTGGAACTCTGGGGCAAGACATGT  
CTATGGTAGCTGAGCCAAACACGTAGGATTTCCGTTTTAAGGTTACATGGAAAAGGTTATAGCTTGG  
CCTTGAGATTGACTCATTAAATCAGAGACTGTAACAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCG  
ACTCTAGAGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCACTTGTATTGTCAGCTTATAATG

## **FIGURE 4**

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFASFCTMFELIIFEILGV  
LNSSSRFYHWMNLCVILLILVFMVPFYIGYFIVSNIRLLHKQRLLEFSCLLWLTMYFFWKL GDP  
FPILSPKHGILSIEQLISRVGVIGVTLMALLSGFGAVNCPYTYMSYFLRNVTDTDILALERLLQ  
TMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSENLTLIQQEVDAL EELSRQ  
LFLETADLYATKERIEYSKTFKGKYNFLGYFFSIYCVWKIFMATINIVFDRVGKTD PVTRGIEI  
TVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAISSSKSSNVIVLLLAQIMGY  
FVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSALSSILFLYLAHKQAPEKQMAP

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **Potential transmembrane domains:**

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,  
425-444

#### **N-glycosylation sites.**

amino acids 67-70, 180-183 and 243-246

#### **Eukaryotic cobalamin-binding proteins**

amino acids 151-160



## FIGURE 5

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGTTCC  
AGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATCTGAGGT  
GTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACT  
TCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGT  
GTCATGCAGAATTATGGGGATCACCTTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTACAG  
AAGCTAAGGAGGCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCC  
TTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTTCGTGGTCATCTCTAG  
GATTAGCCCAACCCCAAGTGTGGGAAAAATGGGTGGGTGTCTGATTGGAAGTTCCAGTGA  
GCCGACAGTTTGCAGCCTATTGTTACAACATCTGATACTTGGACTAAGTTCGTGCATTCCAGAA  
ATTATCACCACCAAAGATCCCATATTCAACACTCAAACGCAACACAAACAGAAATTTATTGT  
CAGTGACAGTACCTACTCGTGGCATCCCTTACTCTACAATACCTGCCCTACTACTACTCCTC  
CTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTGTGTGCACAGAAGTTTATG  
GAACTAGCACCATTGTCTACAGAACTGAACATTTGTTGAAATAAAGCAGCATTAAGAATGA  
AGCTGCTGGGTTTGGAGGTGTCCACGGCTCTGCTAGTGTCTGCTCTCTCTTTGGTGCTG  
CAGCTGGTCTTGGATTTTGTCTATGTCAAAGGTATGTGAAGGCTTCCCTTTTACAAACAAGAAT  
CAGCAGAAGGAAATGATCGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCTAA  
TGAGGAATCAAAGAAAACGTATAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAACTACCGTGC  
GATGCTGGAAGCTGAAGTTTACATGAGACAGAAATGAGGAGACACCTGAGGCTGGTTCCTT  
CATGCTCCTTACCCTGCCAGCTGGGGAATCAAAGGGCCAAAGAACCAAGAAGAAAGTCCA  
CCCTTGGTTCCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAT  
GCCCTTCTCCTTATTGTAACCTGTCTGGATCCTATCCTACCTCCAAAGCTTCCACGGCCT  
TTCTAGCCTGGCTATGTCTAATAATATCCCACTGGGAGAAAGGAGTTTGCAAAGTGCAAGGAC  
CTAAACATCTCATCAGTATCCAGTGGTAAAAGGCCCTCCTGGCTGTCTGAGGCTAGTGGGTTG  
AAAGCCAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCCGCAGCTCAGACCTTTCTTCA  
GCTCTGAAAGAGAAACACGTATCCACCTGACATGTCTTCTGAGCCCGGTAAGAGCAAAAGAAT  
GGCAGAAAAGTTAGCCCCGAAAGCCATGGAGATTCTCATACTTGAGACCTAATCTCTGTAAA  
GCTAAAAATAAGAAATAGAACAAGGCTGAGGATACGACAGTACACTGTCAGCAGGGACTGTAAAC  
ACAGACAGGGTCAAAGTGTCTCTGAACACATTGAGTTGGAATCACTGTTTAGAACACACACA  
CTTACTTTTTCTGGTCTCTACCACTGCTGATATTTCTCTAGGAAATATACTTTTACAAGTAACA  
AAAAATAAACTCTTATAAATTTCTATTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATT  
ACTCAGTAATTTGTTAAAAAGTAATAAAATTCACAAACATTTGCTGAATAGCTACTATATGTC  
AAGTGCTGTGCAAGGTATTACACTCTGTAATTGAATATTATCCTCAAAAAATTGCACATAGTAG  
AACGCTATCTGGGAAGCTATTTTTTTCAGTTTGTATTTCTAGCTTATCTACTTCCAACTAAT  
TTTTATTTTTGCTGAGACTAATCTTATTCATTTCTCTAATATGGCAACCATTATAACCTTAATT  
TATTATTAACATACCTAAGAAGTACATTGTTACCTCTATATACCAAGCACATTTTAAAGTGCC  
ATTAACAAATGTATCACTAGCCCTCCTTTTTCCAACAAGAAGGACTGAGAGATGCAGAAATATT  
TGTGACAAAAAATTAAAGCATTAGAAAACCTT

## **FIGURE 6**

MARCFSLVLLLSIWTTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLG  
LSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYN  
SSDTWTNSCIPEIIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTTPPAPASTSIPR  
RKKLICVTEVFMETSTMSTETETEPFVENKAAFKNEAAGFGGVP TALLVLALLFFGAAAGLGFCYVK  
RYVKAFPFTNKNQOKEMIETKVVKEEKANDSNPNNEESKKT DKNPEESKSPSKTTVRCLEAEV

### **Signal sequence:**

amino acids 1-16

### **Transmembrane domain:**

amino acids 235-254

### **N-glycosylation site.**

amino acids 53-57, 130-134, 289-293

### **Casein kinase II phosphorylation site.**

amino acids 145-149, 214-218

### **Tyrosine kinase phosphorylation site.**

amino acids 79-88

### **N-myristoylation site.**

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

## FIGURE 7

CGCCGCGCTCCCGCACCCGCGGCCCGCCACCGCGCCGCTCCCGCATCTGCACCCGAGCCCGGC  
GGCCTCCCGGCGGGAGCGAGCAGATCCAGTCCGGCCCGCAGCGCAACTCGGTCCAGTCCGGGCGG  
CGGCTGCGGGCGCAGAGCGGAGATGCGAGCGGCTTGGGGCCACCCTGCTGTGCCTGCTGCTGGCGG  
CGGCGGTCCCCACGGCCCCGCGCCCGCTCCGACGCGGACCTCGGCTCCAGTCAAGCCCGGCCCG  
GCTCTCAGCTACCCGCGAGGAGGAGGCCACCCTCAATGAGATGTTCCGCGAGGTTGAGGAACATGAT  
GGAGGACACGCGAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGGCAGAAGAAGCTGCTGCTA  
AAGCATCATCAGAAGTGAACCTGGCAAACCTTACCTCCCAGCTATCACAATGAGACCAACACAGAC  
ACGAAGGTTGGAAATAATACCATCCATGTGCACCGAGAAATTCACAAGATAACCAACAACAGAC  
TGGACAAATGGTCTTTTCAGAGACAGTTATCACATCTGTGGGAGACGAAGAAGGCAGAAGGAGCC  
ACGAGTGCATCATCGACGAGGACTGTGGGCCCAGCATGTACTGCCAGTTTGCCAGCTTCCAGTAC  
ACCTGCCAGCCATGCCGGGGCCAGAGGATGCTCTGCACCCGGGACAGTGAAGTGTGTGGAGACCA  
GCTGTGTGTCTGGGGTCACTGCACCAAAATGGCCACCAGGGGCAGCAATGGGACCATCTGTGACA  
ACCAGAGGGGACTGCCAGCCGGGGCTGTGCTGTGCCCTTCCAGAGAGGCTGCTGTTCCCTGTGTGC  
ACACCCCTGCCCGTGGAGGGCGAGCTTTGCCATGACCCCGCCAGCCGGCTTCTGGACCTCATCAC  
CTGGGAGCTAGAGCCTGATGGAGCCTTGGACCGATGCCCTTGTGCCAGTGGCCTCCTCTGCCAGC  
CCCACAGCCACAGCCTGGTGTATGTGTGAAGCCGACCTTCGTGGGGAGCCGTGACCAAGATGGG  
GAGATCCTGTGCCAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTTCATGGAGGAGGTGCG  
CCAGGAGCTGGAGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGGAGCCTGCGGCTG  
CCGCCGCTGCACTGCTGGGAGGGGAAGAGATTAGATCTGGACCAGGCTGTGGGTAGATGTGCAA  
TAGAAATAGCTAATTTATTTCCCGAGGTGTGTGCTTTAGGCGTGGGCTGACCAGGCTTCTTCCTA  
CATCTTCTTCCAGTAAGTTTCCCCTCTGGCTTGACAGCATGAGGTGTGTGCAATTTGTTTCAGCT  
CCCCAGGCTGTTCTCCAGGCTTACAGTCTGGTGTCTGGGAGAGTCAGGCAGGGTTAAACTGCA  
GGAGCAGTTTGCCACCCCTGTCCAGATTATTTGGCTGCTTTGCCTCTACCAGTTGGCAGACAGCCG  
TTTGTTCTACATGGCTTTGATAATTGTTTGAGGGGAGGAGATGGAACAATGTGGAGTCTCCCTC  
TGATTGGTTTTGGGAAATGTGGAGAAGAGTGCCCTGCTTTGCAAACATCAACCTGGCAAAAATG  
CAACAAATGAATTTCCACGCAGTTCTTTCCATGGGCATAGGTAAGCTGTGCCTTCAGCTGTTGC  
AGATGAAATGTTCTGTTACCCCTGCATTACATGTGTTTATTCATCCAGCAGTGTTGCTCAGCTCC  
TACCTCTGTGCCAGGGCAGCATTTTCATATCCAAGATCAATTCCCTCTCTCAGCACAGCCTGGGG  
AGGGGGTCATTGTTCTCCTCGTCCATCAGGGATCTCAGAGGCTCAGAGACTGCAAGCTGCTTGCC  
CAAGTCACACAGCTAGTGAAGACCAGAGCAGTTTTCATCTGGTTGTGACTCTAAGCTCAGTGCTCT  
CTCCACTACCCACACAGCCTTGGTGCCACCAAAAGTGCTCCCCAAAAGGAAGGAGAATGGGAT  
TTTTCTTGAGGCATGCACATCTGGAATTAAGGTCAAACATAATTCTCACATCCCTCTAAAAGTAAA  
CTACTGTTAGGAACAGCAGTGTCTCACAGTGTGGGGCAGCCGTCTTCTAATGAAGACAATGAT  
ATTGACACTGTCCCTCTTTGGCAGTTGCATTAGTAACCTTGAAAGGTATATGACTGAGCGTAGCA  
TACAGGTTAACCTGCAGAAACAGTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTTGC  
AAAATCACTTAGCAGCAACTGAAGACAATTATCAACCACGTGGAGAAAAATCAAACCGAGCAGGGC  
TGTGTGAAACATGGTTGTAATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAAATGATG  
TTTTCAGGTGTCATGGACTGTTGCCACCATGTATTTCATCCAGAGTTCTTAAAGTTTAAAGTTGCA  
CATGATTGTATAAGCATGCTTTCTTTGAGTTTAAATTATGTATAAACATAAGTTGCATTTAGAA  
ATCAAGCATAAATCACTTCAACTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 8**

MQRLGATLLCLLLAAVPTAPAPAPTATSAPVKPGPALSYQEEATLNEMFREVEELMEDTQHKL  
RSAVEEMEAEAAAASSEVNLANLPPSYHNETNTDTKVGNNTIHVHREIHKITNNQTGQMFSE  
TVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRLCTRDSECCGDQLCVWGHC  
TKMATRGSNGTICDNQRDCQPLCCAFQRGLLFPVCTPLPVEGELCHDPASRLDLITWELEPDG  
ALDRPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEVGSFMEEVRQLELDLE  
RSLTEEMALGEPAAAAAALLGGEET

### **Signal sequence:**

amino acids 1-19

### **N-glycosylation site.**

amino acids 96-100, 106-110, 121-125, 204-208

### **Casein kinase II phosphorylation site.**

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,  
327-331

### **N-myristoylation site.**

amino acids 202-208, 217-223

### **Amidation site.**

amino acids 140-144

## FIGURE 9

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCCAC  
GGCCCACCTTGTGAACCTCGTGCCAGGGCTGATGTGCGTCTTCCAGGGCTACTCATCCAAAG  
GCCTAATCCAACGTTCTGTCTTCAATCTGCAAATCTATGGGGTCTGGGGCTCTTCTGGACCCTT  
AACTGGGTACTGGCCCTGGGCCAATGCGTCTCGCTGGAGCCTTTGCCTCCTTCTACTGGGCCTT  
CCACAAGCCCCAGGACATCCCTACCTTCCCCTTAATCTCTGCCTTCATCCGCACACTCCGTTACC  
ACACTGGGTCAATTGGCATTGAGCCCTCATCCTGACCCTTGTGCAGATAGCCCGGTTCATCTTG  
GAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCCTGTAGCCCGCTGCATCATGTGCTGTTT  
CAAGTGCTGCCCTCTGGTGTCTGGAAAAATTTATCAAGTTCCTAAACCGCAATGCATACATCATGA  
TCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAAAATGCGTTCATGCTACTCATGCGAAAC  
ATTGTCAGGGTGGTCGCTCTGGACAAAGTCACAGACCTGCTGCTGTTCTTTGGGAAGCTGCTGGT  
GGTCGGAGGCGTGGGGTCTCTGCTTCTTTTTTTCTCCGGTCGCATCCCGGGGCTGGGTAAAG  
ACTTTAAGAGCCCCACCTCAACTATTACTGGCTGCCCATCATGACCTCCATCCTGGGGGCCTAT  
GTCATCGCCAGCGGCTTCTTCAGCGTTTTTCGGCATGTGTGTGGACACGCTCTTCCTCTGCTTCCT  
GGAAGACCTGGAGCGGAACAACGGCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAA  
AGATTCTGGGCAAGAAGAACGAGGCGCCCCCGGACAACAAGAAGAGGAAGAAGTGACAGCTCCGG  
CCCTGATCCAGGACTGCACCCACCCACCGTCCAGCCATCCAACCTCACTTCGCCTTACAGGT  
CTCCATTTTGTGGTAAAAAAGGTTTTAGGCCAGGCGCCGTGGCTCACGCCTGTAATCCAACACT  
TTGAGAGGCTGAGGCGGGCGGATCACCTGAGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTG  
AAACCTCCGTCTCTATTAATAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCATCCCA  
GCTACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCGGGAGGCAGAGGTTGCAGTGAGCCGA  
GATCGCGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAAACAAA  
AAGATTTTATTAAAGATATTTTGTAACTC

## **FIGURE 10**

RTRGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVLGGLFWTL  
NWLALGQCVLGAFASFYWAFHKPQDIPTFPLISAFIRTLRYHTGSLAFGALILTLVQIARVIL  
EYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAKNAFMLLMRN  
IVRVVVLDKVTDLLFFGKLLVVGVGVLSEFFFFSGRIPGLGKDFKSPHLNYYWLPIMTSILGAY  
VIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYYSKSLKILGKKNEAPPDNKKRKK

### **Important features:**

#### **Transmembrane domains:**

amino acids 57-80 (type II), 110-126, 215-231, 254-274

#### **N-glycosylation sites.**

amino acids 16-20, 27-31, 289-293

#### **Hypothetical YBR002c family proteins.**

amino acids 276-288

#### **Ammonium transporters proteins.**

amino acids 204-231

#### **N-myristoylation sites.**

amino acids 60-66, 78-84

#### **Amidation site.**

amino acids 306-310

## FIGURE 11

GCCCCGCGCCCGGCGCCGGGCGCCCCGAAGCCGGGAGCCACCGCCATGGGGGCCTGCCTGGGAGCCTGC  
TCCCTGCTCAGCTGCGCGTCTGCCTCTGCGGCTCTGCCCCCTGCATCCTGTGCAGCTGCTGCCCCG  
CAGCCGCAACTCCACCGTGAGCCGCTCATCTTACGTTCTTCTCTTCTGCGGGTGCTGGTGTCCA  
TCATTATGCTGAGCCCGGGCGTGGAGAGTCAGCTCTACAAGCTGCCCTGGGTGTGTGAGGAGGGGGC  
GGGATCCCCACCGTCTGCAGGGCCACATCGACTGTGGCTCCCTGCTTGGCTACCGCGCTGTCTACCG  
CATGTGCTTCGCCACGGCGGCTTCTTCTTCTTCTTTTACCCTGCTCATGCTCTGCGTGAGCAGCA  
GCCGGGACCCCCGGGTGCCATCCAGAATGGGTTTTGGTTCTTTAAGTTCCTGATCCTGGTGGGCCTC  
ACCGTGGGTGCCTTCTACATCCCTGACGGCTCCTTACCAACATCTGGTTCTACTTCGGCGCTCGTGGG  
CTCCTTCTCTTTCATCCTCATCCAGCTGGTGTGCTCATCGACTTTGCGCACTCCTGGAACACGCGGT  
GGCTGGGCAAGGCCGAGGAGTGCATTCCCGTGCTGGTACGCAGGCCTTCTTCTTCTACTCTCCTC  
TTCTACTTGCTGTGATCGCGCCGTGGCGCTGATGTTTATGTACTACTGAGCCCAGCGGTGCCA  
CGAGGGCAAGGTCTTCATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGTCCATCGCTGCTGCTGCTG  
CCAAGGTCCAGGACGCCAGCCAACTCGGGTCTGCTGCAGGCCTCGGTTCATCACCTCTACACCATG  
TTTGTACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCAACCCCCATTGCCAACCCAGCT  
GGGCAACGAGACAGTTGTGGCAGGCCCCGAGGGCTATGAGACCCAGTGGTGGGATGCCCCGAGCATTG  
TGGGCCTCATCATCTTCTCTCTGTGCACCCTCTTCATCAGTCTGCGCTCCTCAGACCACCGGCAGGTG  
AACAGCCTGATGCAGACCGAGGAGTGCCACCTATGCTAGACGCCACACAGCAGCAGCAGCAGCAGGT  
GGCAGCCTGTGAGGGCCGGGCTTTGACAACGAGCAGGACGGCGTCACCTACAGTACTCCTTCTTCC  
ACTTCTGCCTGGTGTGCGCTCACTGCACGTATGATGACGCTCACCAACTGGTACAAGCCCGGTGAG  
ACCCGGAAGATGATCAGCAGCTGGACCGCGTGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCT  
CCTCTACCTGTGGACCCTGGTAGCCCCACTCCTCCTGCGCAACCGCGACTTCAGCTGAGGCAGCCTCA  
CAGCCTGCCATCTGGTGCCTCCTGCCACCTGGTGCCTCTCGGCTCGGTGACAGCCAACCTGCCCCCTC  
CCACACCAATCAGCCAGGCTGAGCCCCCACCCTGCCCCAGCTCCAGGACCTGCCCCTGAGCCGGGC  
CTTCTAGTCGTAGTGCCCTCAGGGTCCGAGGAGCATCAGGCTCCTGCAGAGCCCCATCCCCCGCCAC  
ACCCACACGGTGGAGCTGCCTCTTCTTCCCCCTCCTCCTGTTGCCATACTCAGCATCTCGGATGAA  
AGGGCTCCCTTGTCTCAGGCTCCACGGGAGCGGGGCTGCTGGAGAGAGCGGGGAACCTCCACACAG  
TGGGGCATCCGGCACTGAAGCCTGGTGTCTCTGGTCACGTCCCCAGGGGACCCTGCCCCCTTCTG  
GACTTCGTGCCTTACTGAGTCTCTAAGACTTTTTCTAATAACAAGCCAGTGCCTGTAAAAAAA

## **FIGURE 12**

MGACLGACSLSCASCSCGSA PCILCSCCPASRNSTVSRLIFTFFLFLGVLVSIIMLSPGVESQL  
YKLPWVCEEGAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFFFTLLMLCVSSSRDPRAAIQ  
NGFWFFKFLIILVGLTVGAFYIPDGSFTNIWFYFGVVGSELFILIQVLVLLIDFAHSWNQRWLKAE  
ECDSRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFISLNLTFVCVVSIAAVLPKV  
QDAQPNSGLLQASVITLYTMEVTWSALSSIPEQKCNPHLPTQLGNETVVAGPEGYETQWWDAPSI  
VGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQVAACEGRAFDNEQDGVITYSY  
SFFHFCLVLASLHVMMTLTNWYKPGETRMISTWTAVVVKICASWAGLLLYLWTLVAPLLLRNRD  
FS

### **Signal sequence:**

amino acids 1-20

### **Transmembrane domains:**

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,  
272-283, 324-340, 391-406, 428-444



### FIGURE 13

CGGGCCAGCCTGGGGCGGCCGCGCCAGGAACCCGTTAAGGTGTCTTCTCTTTAGGGATGGTGA  
GGTTGGAAAAAGACTCCTGTAACCCCTCCTCCAGGATGAACCACCTGCCAGAAGACATGGAGAACG  
CTCTCACCAGGAGCCAGAGCTCCCATGCTTCTCTGCGCAATATCCATTCCATCAACCCACACAA  
CTCATGGCCAGGATTGAGTCCTATGAAGGAAGGGAAAAGAAAGGCATATCTGATGTCAGGAGGAC  
TTTCTGTTTGTGTCACCTTTGACCTCTTATTCGTAACATTACTGTGGATAATAGAGTTAAATG  
TGAATGGAGGCATTGAGAACACATTAGAGAAGGAGGTGATGCAGTATGACTACTATTCTTCATAT  
TTTGATATATTCTTCTGGCAGTTTTTCGATTTAAAGTGTTAATACTTGCATATGCTGTGTGCAG  
ACTGCGCCATTGGTGGGCAATAGCGTTGACAACGGCAGTGACCAGTGCCTTTTTACTAGCAAAAG  
TGATCCTTTTGAAGCTTTTCTCTCAAGGGGCTTTTGGCTATGTGCTGCCCATCATTTCATTCATC  
CTTGCCCTGGATTGAGACGTGGTTTCTGGATTTCAAAGTGTTACCTCAAGAAGCAGAAGAAGAAAA  
CAGACTCCTGATAGTTTCAAGATGCTTCAGAGAGGGCAGCACTTATACCTGGTGGTCTTTCTGATG  
GTCAGTTTTTATCCCTCCTGAATCCGAAGCAGGATCTGAAGAAGCTGAAGAAAAACAGGACAGT  
GAGAAACCACTTTTAGAACTATGAGTACTACTTTTGTTAAATGTGAAAAACCCTCACAGAAAGTC  
ATCGAGGCAAAAAGAGGCAGGCAGTGGAGTCTCCCTGTCGACAGTAAAGTTGAAATGGTGACGTC  
CACTGCTGGCTTTATTGAACAGCTAATAAAGATTTATTATTGTAATACCTCACAAACGTTGTAC  
CATATCCATGCACATTTAGTTGCCTGCCTGTGGCTGGTAAGGTAATGTCATGATTCATCCTCTCT  
TCAGTGAGACTGAGCCTGATGTGTTAACAATAGGTGAAGAAAGTCTTGTGCTGTATTCTTAATC  
AAAAGACTTAATATATTGAAGTAACACTTTTTTAGTAAGCAAGATACCTTTTTATTTCATTAC  
AGAATGGAATTTTTTGTTCATGTCTCAGATTTATTTGTATTTCTTTTTTAACACTCTACATT  
TCCCTTGTTTTTTAACTCATGCACATGTGCTCTTTGTACAGTTTTAAAAAGTGAATAAAATCTG  
ACATGTCAATGTGGCTAGTTTTATTTCTGTTTGCATTATGTGTATGGCCTGAAGTGTGGA  
CTTGCAAAAGGGGAAGAAAGGAATTGCGAATACATGTAAATGTCACCAGACATTTGTATTATTT  
TTATCATGAAATCATGTTTTCTCTGATTGTTCTGAAATGTTCTAAATACTCTTATTTTGAATGC  
ACAAAATGACTTAAACCATTATATCATGTTTCCTTTGCGTTCAGCCAATTTCAATTAAATGAA  
CTAAATTAAAAA

## **FIGURE 14**

MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVTFDLLF  
VTLLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIALTT  
AVTSAFLLAKVILSKLFSQGAFGYVLPPIISFILAWIETWFLDFKVLQPQEAEEENRLLIVQDASER  
AALIPGGLSDGQFYSPPESEAGSEEAEKQDSEKPLLEL

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-20

#### **Transmembrane domains:**

amino acids 54-72, 100-118, 130-144, 146-166

#### **N-myristoylation sites.**

amino acids 14-20, 78-84, 79-85, 202-208, 217-223

## FIGURE 15

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCGACCCGCCAGGAAAGACTGAGG  
 CCGCGGCTGCCCGCCCGGCTCCCTGCGCCGCGCGCCCTCCCGGGACAGAAGATGTGCTCCAG  
 GGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCTGGGGCCTGGGGTGCAGGGCTGCCCAT  
 CCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCTGCACTGCCCGCCAGGGGACCCACGGTGCCC  
 CGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCTTTGAGAACGGCATCACCATGCTCGACGC  
 AGGCAGCTTTGCGGCCCTGCCGGGCTGAGCTCCTGGACCTGTCACAGAACCAGATCGCCAGCC  
 TGCCAGCGGGGTCTTCCAGCCACTCGCCAACCTCAGCAACCTGGACCTGACGGCCAACAGGCTG  
 CATGAAATCACCAATGAGACCTTCCGTGGCCTGCGGCGCTCGAGCGCCTCTACCTGGGCAAGAA  
 CCGCATCCGCCACATCCAGCCTGGTGCTTCGACACGCTCGACCGCTCCTGGAGCTCAAGCTGC  
 AGGACAACGAGCTGCGGGCACTGCCCGGCTGCGCCTGCCCGCCTGCTGCTGCTGACCTCAGC  
 CACAACAGCCTCCTGGCCCTGGAGCCCGGCATCCTGGACACTGCCAACGTGGAGGCGCTGCGGCT  
 GGCTGGTCTGGGGCTGCAGCAGCTGGACGAGGGGCTCTCAGCCGCTTGCGCAACCTCCACGACC  
 TGGATGTGTCCGACAACAGCTGGAGCGAGTGCCACCTGTGATCCGAGGCTCCGGGGCTGACG  
 CGCCTGCGGCTGGCCGGCAACACCCGCATTGCCAGCTGCGGCGCGAGGACCTGGCCGGCTGGC  
 TGCCCTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGCGCTGCTGGCGACCTCTCGGGCC  
 TCTTCCCCCGCTGCGGCTGCTGGCAGCTGCCCGCAACCCCTTCAACTGCGTGTGCCCCCTGAGC  
 TGTTTGGCCCTGGGTGCGGAGAGCCAGTCACTAGGCCAGCCCTGAGGAGACCGCTGCCA  
 CTTCGCCCAAGAACGCTGGCCGGCTGCTCCTGGAGCTTACTACGCCGACTTTGGCTGCCAG  
 CCACCACCACACAGCCACAGTGGCCACCAGAGGCCCGTGGTGCGGGAGGCCACAGCCTTGCTCT  
 TCTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCGCGCCACTGAGGCCCGGCGCCCTC  
 CACTGCCCCACCGACTGTAGGGCTGTCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCTCA  
 ATGGGGGCACATGCCACCTGGGGACACGGCACCACTGGCGTGCTTGTGCCCCGAAGGCTTCAGG  
 GGCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACGGCCAGCCCTACACCAGTCAACGCCAG  
 GCCACCACGGTCCCTGACCTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGC  
 AGCGCTACCTCCAGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTACCTATCGCAACCTATCG  
 GGCCCTGATAAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCACCCA  
 GCTGCGGCCCCAACGCCACTTACTCCGTCTGTGTGTCGCTTTGGGGCCCGGGCGGGTGCCGAGG  
 GCGAGGAGGCTGCGGGGAGGCCATACACCCCGAGCCGTCCACTCCAACCAGCCCCAGTCAAC  
 CAGGCCCGCGAGGGCAACCTGCCGCTCCTCATTGCGCCGCGCTGGCCGCGGTGCTCCTGGCCGC  
 GCTGGCTGCGGTGGGGGAGCCTACTGTGTGCGGCGGGGGCGGGCCATGGCAGCAGCGGCTCAGG  
 ACAAGGGCAGGTGGGGCCAGGGGCTGGGCCCCGGAAGTGGAGGGAGTGAAGTCCCCCTGGAG  
 CCAGGCCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGGTCTGAGTGTGAGGTGCC  
 ACTCATGGGCTTCCCAGGGCTGGCCTCCAGTCAACCCCTCCACGCAAGGCCCTACATCTAAGCCA  
 GAGAGAGACAGGGCAGCTGGGGCGGGCTCTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCC  
 ACACCACGTAAGTTCTCAGTCCCAACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCT  
 GGGCCCTGTTCCCTCTGGACCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCC  
 CTAACGTCCCCAGAACCAGTGCCTATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTC  
 CCTGGGCACGGCGGGCCCTGCCATGTGCTGGTAACGCATGCCTGGGTCTGCTGGGCTCTCCAC  
 TCCAGGCGGACCCTGGGGGCAAGTGAAGGAAGCTCCCGAAAAGAGCAGAGGGAGAGCGGGTAGGC  
 GGCTGTGTGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAGGAAGATGC  
 TTTAGGAACATGTTTTGCTTTTTTAAATATATATATTATAAGAGATCCTTTCCCATTTATTCT  
 GGAAGATGTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTGTAGACAAACGATGATATGAA  
 GGCTTTTTGTAGAAAAAATAAAGATGAAGTGTGAAA

## **FIGURE 16**

MCSRVPLLLLLLLLLALGPGVQGCPSGCQCSQPQTTFCTARQGTTPRDVPPDTVGLYVFENGIT  
MLDAGSFAGLPGLQLLDLSQNIASLPSGVFQPLANLSNLDLTANRLHEITNETFRGLRRLERLY  
LGKNRIRHIQPGAFDTLDRLELKLQDNELRALPPLRLPRLLLLDLSHNSLLALEPGILDANVE  
ALRLAGLGLQQLDEGLFSRLRLNLDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQLRPEDL  
AGLAALQELDVSNLSLQALPGDLSGLFPRLRLLLAAARNPFNCVCPLSWFGPWVRESHVTLASPEE  
TRCHFPPKNAGRLLLELDYADFGCPATTTTATVPPTTRPVVREPTALSSSLAPTWLSPTAPATEAP  
SPPSTAPPTVGFVPQPDQCPSTCLNGGTCHLGRHHLACLCPEGFTGLYCESQMGQGRPSPTP  
VTPRPPRSLTLGIEPVSPSTLRVGLQRYLQSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEY  
TVTQLRPNATYSVCMPLGPRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAV  
LLAALAAVGAAYCVRGRAMAAAAQDKGQVGPAGPLELEGVKVPLEPGPKATEGGGEALPSGSE  
CEVPLMGFPGLQSPHAKPYI

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **Transmembrane domain:**

amino acids 579-599

#### **EGF-like domain cysteine pattern signature.**

amino acids 430-442

#### **Leucine zipper pattern.**

amino acids 197-219, 269-291

#### **N-glycosylation sites.**

amino acids 101-105, 117-121, 273-277, 500-504, 528-532

#### **Tyrosine kinase phosphorylation sites.**

amino acids 124-131, 337-345

#### **N-myristoylation sites.**

amino acids 23-29, 27-33, 70-76, 142-148, 187-193, 348-354,  
594-600, 640-646

[illegible][illegible]

## **FIGURE 18**

MRVRIGLTLLLCAVLLSLASASSDEEGSQDESLSKTTLTSDSVKDHTTAGRVVAGQIFLDSESEL  
ESSIQEEEDSLKSQEGESVTEDISFLESPNPENKDYEEPKKVRKPALTAIEGTAHGEPCHFPLFLDK  
EYDECTSDGREDGRLWCATTYDYKADEKWGFCETEEEAARRQMQEAEMMYQTGMKILNGSNKKSQKR  
EAYRYLQKAASMNHTKALERVSYALLFGDYLPQNIQAAREMFEEKLTEEGSPKGQTALGFLYASGLGVN  
SSQAKALVYYTFGALGGNLIAMVLSRL

### **Important features:**

#### **Signal peptide:**

amino acids 1-21

#### **N-glycosylation sites.**

amino acids 195-199, 217-221, 272-276

#### **Tyrosine kinase phosphorylation site.**

amino acids 220-228

#### **N-myristoylation sites.**

amino acids 120-126, 253-259, 268-274, 270-274, 285-291, 289-295

#### **Glycosaminoglycan attachment site.**

amino acids 267-271

#### **Microbodies C-terminal targeting signal.**

amino acids 299-303

#### **Type II fibronectin collagen-binding domain protein.**

amino acids 127-169

#### **Fructose-bisphosphate aldolase class-II protein.**

amino acids 101-119

## FIGURE 19

AATTCAGATTTTAAGCCCATCTGTCAGTGAATTTTCATGAACTAGCAAGAGGACACCATCTTCTT  
GTATTATACAAGAAAGGAGTGACCTATCACACACAGGGGAAAAATGCTCTTTTGGGTGCTAGG  
CCTCCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAAAACATAAGATTGAAGACATCACTG  
ATAAGTACATTTTTATCACTGGATGTGACTCGGGCTTTGGAACTTGGCAGCCAGAACCTTTTGAT  
AAAAAGGGATTTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAACAGCTTTAAAGGCAGA  
AACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAGAGAATGTCAAGAGGACTG  
CCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGGTCTCTGGGGTCTGATCAATAATGCTGGTGTT  
CCCGGCGTGCTGGCTCCCACTGACTGGCTGACACTAGAGGACTACAGAGAACCTATTGAAGTGAA  
CCTGTTTGGACTCATCAGTGTGACACTAAATATGCTTCCTTTGGTCAAGAAAGCTCAAGGGAGAG  
TTATTAATGTCTCCAGTGTGGAGGTCGCTTGCAATCGTTGGAGGGGGCTATACTCCATCCAAA  
TATGCACTGGAAGGTTTCAATGACAGCTTAAGACGGGACATGAAAGCTTTTGGTGTGCACGTCTC  
ATGCATTGAACCAGGATTGTTCAAAACAACTTGGCAGATCCAGTAAAGGTAATTGAAAAAAAC  
TCGCCATTTGGGAGCAGCTGTCTCCAGACATCAAACAACAATATGGAGAAGGTTACATTGAAAA  
AGTCTAGACAAACTGAAAGGCAATAAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTG  
CATGGACCACGCTCTAACAAGTCTCTTCCCTAAGACTCATTATGCCGCTGGAAGATGCCAAAA  
TTTTCTGGATACCTCTGTCTCACATGCCAGCAGCTTTGCAAGACTTTTATTGTTGAAACAGAAA  
GCAGAGCTGGCTAATCCCAAGGCAGTGTGACTCAGCTAACCACAAATGTCTCCTCCAGGCTATGA  
AATTGGCCGATTTCAAGAACACATCTCCTTTTCAACCCCATTCCTTATCTGCTCCAACCTGGACT  
CATTTAGATCGTGCTTATTTGGATTGCAAAAGGGAGTCCCACCATCGCTGGTGGTATCCCAGGGT  
CCCTGCTCAAGTTTTCTTTGAAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCCTGCCCT  
GTATTTAGGCTTTGCCTGCTTGGTGTGATGTAAGGGAAATTGAAAGACTTGCCCATTCAAATGA  
TCTTTACCGTGGCCTGCCCCATGCTTATGGTCCCAGCATTTACAGTAACTTGTGAATGTTAAGT  
ATCATCTCTTATCTAAATATTTAAAGATAAGTCAACCCAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAA

## **FIGURE 20**

MLFWVLGLLILCGFLWTRKGLKIEDITDKYIFITGCDSGFGNLAARTFDKKG FHVIAACLTESG  
STALKAETSERLRTVLLDVTDPENVKRTAQWVKNOVGEGKLWGLINNAGVPGVLAPTDWLTLEDY  
REPIEVNLFGLISVTLNMLPLVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGFND SLRRDMK  
AFGVHVS CIEPGLFKTNLADP VKVIEKKLAIWEQLSPDIKQQYGE GYIEKSLDKLKG NKSYVNMD  
LSPVVECDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQKAE LANPKAV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 136-152

**N-glycosylation sites.**

amino acids 161-163, 187-190 and 253-256

**Glycosaminoglycan attachment site.**

amino acids 39-42

**N-myristoylation sites.**

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212



## FIGURE 21

CTGAGGCGGCGGTAGCATGGAGGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCGGCG  
CACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTTCTTCTTGGGGAAGTAAAA  
GGTGAAGCCAAGAACAGCATTACTGATTCCCAAATGGATGATGTTGAAGTTGTTTATACAATTGA  
CATTCAAGAAATATATTCCATGCTATCAGCTTTTTAGCTTTTATAATTCTTCAGGCGAAGTAAATG  
AGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGTTGGTACAAATTCCGT  
CGTCATTCAAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAAAACTTGCAAGGAGCATT  
TTCAAACCAAGACCTTGTTTTCTGCTATTAAACCAAGTATAATAACAGAAAGCTGCTCTACTC  
ATCGACTGGAACATTCTTTATATAAACCTCAAAAAGGACTTTTTACAGGGTACCTTTAGTGGTT  
GCCAATCTGGGCATGTCTGAACAACTGGGTATAAACTGTATCAGGTTCTGTATGTCCACTGG  
TTTTAGCCGAGCAGTACAAACACACAGCTCTAAATTTTTGAAGAAGATGGATCCTTAAAGGAGG  
TACATAAGATAAATGAAATGTATGCTTCATTACAAGAGGAATTAAAGAGTATATGCAAAAAGTG  
GAAGACAGTGAACAAGCAGTAGATAAACTAGTAAAGGATGTAAACAGATTAAAACGAGAAATTGA  
GAAAAGGAGAGGAGCACAGATTCAGGCAGCAAGAGAGAAGAACATCCAAAAGACCCTCAGGAGA  
ACATTTTTCTTTGTGAGGCATTACGGACCTTTTTTCCAAATTCCTGAATTTCTTCATTTCATGTGTT  
ATGTCTTTAAAAAATAGACATGTTTCTAAAAGTAGCTGTAACACCAACCACATCTCGATGTAGT  
AGACAATCTGACCTTAATGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCAC  
AAATCATTAAGCATAAAGCCTTAGACTTAGATGACAGATGGCAATTCAAGAGATCTCGGTTGTTA  
GATACACAAGACAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAAAT  
GAGCAGCCCAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTTGGTGAATATTCACGGTCTC  
CTACATTTTGATCCTTTTAACCTTACAAGGAGATTTTTTTATTTGGCTGATGGGTAAAGCCAAAC  
ATTTCTATTGTTTTTACTATGTTGAGCTACTTGACAGTAAGTTCATTTGTTTTTACTATGTTTACC  
TGTTTGAGTAATACACAGATAACTCTTAGTGCATTTACTTCACAAAGTACTTTTTCAAACATCA  
GATGCTTTTATTTCCAAACCTTTTTTTCACCTTTCACCTAAGTTGTTGAGGGGAAGGCTTACACAG  
ACACATTCTTTAGAATTGGAAGAGTGAGACCAGGCACAGTGGCTCACACCTGTAATCCCAGCACT  
TAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCCTGGGCAACGTATT  
GAGACCATGTCTATTAAAAAATAAAATGGAAGCAAGAATAGCCTTATTTTCAAATATGGAAG  
GAAATTTATATGAAAATTTATCTGAGTCATTAAATTCCTTAAGTGATACTTTTTTAGAAGTA  
CATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCAATAAATTTGCAAAACATCATCT  
AAAAATTTAAAAA

## **FIGURE 22**

MEGESTSAVLSGFVLGALAFQHLNTDSDTEGFLLEVKGEAKNSITDSQMDDVEVVYTIDIQKYI  
PCYQLFSFYNSSGEVNEQALKKILSNVKKNVVGWYKFRRHSDQIMTFRERLLHKNLQEHFSNQDL  
VFLLLTPSIITESCSTHRLEHSYKPKGLFHRVPLVVANLGMSEQLGYKTVSGSCMSTGFSRAV  
QTHSSKFFEEEDGSLKEVHKINEMYASLQEEELKSICKKVEDSEQAVDKLVKDVNRLKREIEKRRGA  
QIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSSCNYNHHLDDVVDNLTL  
MVEHTDIPEASPASTPQIIKHKALDLDLDRWQFKRSRLDLDQDKRSKANTGSSNQDKASKMSSPET  
DEEIEKMKGFGEYSRSPTF

**Important features:**

**Signal peptide:**

amino acids 1-19

**N-glycosylation sites.**

amino acids 75-79, 322-326

**N-myristoylation site.**

amino acids 184-154

**Growth factor and cytokines receptors family.**

amino acids 134-150

## FIGURE 23

GGCACAGCCGCGCGCGGAGGGCAGAGTCAGCCGAGCCGAGTCCAGCCGACGAGCGGACCAGCGCAGGGCAGCCCAA  
GCAGCGCGCAGCGAACGCCCGCCGCCGCCACACCTCTGCGGTCCCGCGGCGCCTGCCACCTTCCCTCCTTCCCC  
GCGTCCCCGCTCGCCGCGCAGTCAGCTTGCGGGTTGCTGCCCCGCGAAACCCGAGGTACCAGCCGCGCCTCT  
GCTTCCCTGGGCGCGCGCGCCTCCACGCCCTCCTTCTCCCTGGCCGCGCCTGGCACCAGGGGACCGTTGCGCTGA  
CGCGAGGCCAGCTCTACTTTTCCCCCGCGTCTCCTCGGCTGCTCGCCTCTTCCACCACTCCAACCTCCTTCCC  
TCCAGCTCCACTCGCTAGTCCCCGACTCCGCCAGCCCTCGGCCGCTGCCGTAGCGCCGCTTCCCGTCCGCTCCCAA  
GGTGGGAACGCGTCCGCCCGCGCCGACCAATGCGCACGGTTGCGCTTGCCCGCGCTTCTGTCACCTGGCAGTGCTC  
AGCGCGCGCTGCTGGCTGCCGAGCTCAAGTCGAAAAGTTGCTCGGAAGTGCACGCTTTTACGTGTCAAAGGCTTC  
AACAGAACGATGCCCTCCACGAGATCAACGGTGATCATTGAAGATCTGTCCCAGGGTTCTACCTGCTGCTCT  
CAAGAGATGGAGGAGAAGTACAGCTGCAAGATAAGATGATTTCAAAGTGTGGTCAGCGAACAGTGCAATCATTTG  
CAAGTGTCTTTGCTTACGTTACAAGAAGTTGATGAATCTTCAAAGAAGTACTTGAAGTGCAGAGAAATCCCTG  
AATGATATGTTTGTGAAGACATATGGCCATTTATACATGCAAAATTTGAGCTATTTAAAGATCTCTTCGTAGAGTTG  
AAACGTTACTACGTGGTGGGAAATGTGAACCTGGAAGAAATGCTAAATGACTTCTGGGCTCGCCTCCTGGAGCGGATG  
TTCGCGCTGGTGAACCTCCAGTACCACCTTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAG  
CCCTTCGAGATGTCCCTCGCAAATTAAGCTCCAGGTTACTCGTGCTTTTGTAGCAGCCGTAATTTGCTCAAGGC  
TTAGCGGTTGCGGGAGATGTGCTGAGCAAGTCTCCGTGGTAAACCCACAGCCAGTGTACCCATGCCCTGTTGAAG  
ATGATCTACTGCTCCACTGCCGGGTCTCGTGACTGTGAAGCCATGTTACAAGTACTGCTCAAACATCATGAGAGGC  
TGTTTGGCAACCAAGGGGATCTCGATTTTGAATGGAACAATTTATAGATGCTATGCTGATGGTGGCAGAGAGGCTA  
GAGGGTCCCTTCAACATTGAATCGGTCTGATGATCCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAGGAT  
AATAGTGTCAAGTGTCTCAGAAGTTTCCAGGGATGTGGACCCCCAAGCCCTCCAGCTGGACGAATTTCTCGT  
TCCATCTCTGAAAGTGCTTCACTGCTCGCTTCCAGCCACATCAGCCGAGGAACGCCAACCACAGCAGCTGGCACT  
AGTTTGGACCGACTGGTTACTGATGTCAAGGAGAACTGAAACAGGCCAAGAAATTTCTGGTCTCCCTTCCGAGCAAC  
GTTTGCAACGATGAGAGGATGGCTGCAGGAACGGCAATGAGGATGACTGTTGGAATGGGAAAGGCAAAAGCAGGTAC  
CTGTTTGCACTGACAGGAAATGGATTAGCCAACAGGGCAACAACCCAGAGGTCCAGGTTGACACCAGCAACCCAGAC  
ATACTGATCCTTCGTCAAATCATGGCTCTTCGAGTGTGACCAAGATGAAGAATGCATACAATGGGAACGACGTG  
GACTTCTTTGATATCAGTGATGAAAGTAGTGGAGAAGGAAGTGAAGTGGCTGTGAGTATCAGCAGTGCCCTTCAGAG  
TTTGACTACAATGCCACTGACCATGCTGGGAAGAGTGCCAAATGAGAAAGCCGACAGTGTGTTGCTCGTCTGGGGCA  
CAGGCCCTACCTCCTCACTGTCTTCTGCATCTTGTCTGTTATGCAGAGAGAGTGGAGATAATCTCAAACCTGAG  
AAAAAGTGTTCATCAAAAGTTAAAAGGCACCACTTATCACTTTTCTACCATCCTAGTGACTTTGCTTTTAAATGAA  
TGGACAACAATGTACAGTTTTTACTATGTGGCCACTGGTTTAAAGAGTGTGACTTTGTTTTCTCATTAGTTTTGGG  
AGGAAAAGGACTGTGCATTGAGTTGGTTCCTGCTCCCCAAACCATGTTAAACGTGGCTAACAGTGTAGGTACAGAA  
CTATAGTTAGTTGTGCATTTGTGATTTTATCACTCTATTATTTGTTGTATGTTTTTCTCATTTCGTTTGTGGGTT  
TTTTTTTCCAACGTGATCTCGCCTTGTTCCTTACAAGCAAAACAGGGTCCCTTCTTGGCACGTAACATGTACGTATT  
TCTGAAATATTAATAGCTGTACAGAAGCAGGTTTTATTATCATGTTATCTTATTAAGAAAAAGCCCAAAAGC

## **FIGURE 24**

MARFGLPALLCTLAVLSAALLAAELKSKSCSEVRRRLVSKGFNKNDAPLHEINGDHLKICPQGST  
CCSQEMEKEYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMFVKTYGH  
LYMQNSELFKDLFVELKRYVVGNVNLEEMLNDFWARLLERMFRLVNSQYHFTDEYLECVSKYTE  
QLKPFQDVPRKLLQVTRAFVAARTFAQGLAVAGDVSKVSVVNPTAQCTHALLKMIYCSHCRL  
VTVKPCYNYCSNIMRGCLANQGDLD FEWNNFIDAMLMVAERLEGPFNIESVMDPIDVKISDAIMN  
MQDNSVQVSQKVFQCGPPKPLPAGRISRSISESAFSARFRPHHPEERPTTAAGTSLDRLVTDVK  
EKLKQAKKFWSSLP SNVCNDERMAAGNGNEDDCWNGKGKSRYLEFAVTGNGLANQGNNEVQVDTIS  
KPDILILRQIMALRVMTSKMKNAYNGNDVDFDISDESSGEGSGSGCEYQQCPSEFDYNATDHAG  
KSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

### **Important features:**

#### **Signal peptide:**

amino acids 1-22

#### **ATP/GTP-binding site motif A (P-loop).**

amino acids 515-524

#### **N-glycosylation site.**

amino acids 514-518

#### **Glycosaminoglycan attachment sites.**

amino acids 494-498, 498-502

#### **N-myristoylation sites.**

amino acids 63-69, 224-230, 276-282, 438-444, 497-503, 531-537

#### **Glypicans proteins.**

amino acids 54-75, 105-157, 238-280, 309-346, 423-460, 468-506

## FIGURE 25

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCTGAC  
CTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAAGCAACT  
TACAGCTGCACCGACAGTTGCGATGAAAGTTCTAATCTCTTCCCTCCTCCTGTTGCTGCCACTAA  
TGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTCGCCAGAGGCCACAGGGACCGAGGC  
CAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAAAGATTGGTTCCTGAG  
AGCCCCGAGAAGAAAATTTCATGACAGTGTCTGGGCTGCCAAAGAAGCAGTGCCCCCTGTGATCATT  
TCAAGGGCAATGTGAAGAAAACAAGACACCAAGGCACCACAGAAAGCCAAACAAGCATTCCAGA  
GCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTTTGCTCTGCCTTTGTAGGAGCTCTG  
AGCGCCCACTCTTCCAATTAAACATTCTCAGCCAAGAAGACAGTGAGCACACCTACCAGACACTC  
TTCTTTCTCCCACTCACTCTCCCACTGTACCCACCCCTAAATCATTCCAGTGCTCTCAAAAAGCA  
TGTTTTTCAAGATCATTTTGTGTTGTTGCTCTCTCTAGTGTCTTCTCTCTCGTCAGTCTTAGCCT  
GTGCCCTCCCCCTTACCCAGGCTTAGGCTTAATTACCTGAAAGATTCCAGGAAACTGTAGCTTCCT  
AGCTAGTGTCAATTTAACCTTAAATGCAATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTTTT  
AAATGTCAAAAAAAAAAAAAAAAAA

## **FIGURE 26**

MKVLISLLLLLLPLMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRRKFM  
TVSGLPKKQPCDHFKNVKKTRHQRHHRKPNKHSRACQQFLKQCQLRSFALPL

**Important features:**

**Signal peptide:**

amino acids 1-22

**N-myristoylation sites.**

amino acids 27-33, 46-52

## FIGURE 27

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCTCAG  
AGCTGGTCTGCCATGGACATCCTGGTCCCACTCCTGCAGCTGCTGGTGTGCTTCTTACCCTGCC  
CCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCCCTGTGCAAAAGCTACTTCCCCCTACCTGA  
TGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAGCTCTTCAGCCAG  
ATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTACTGGAGCTGGGCTGCGGAACCGGAGC  
CAACTTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACCCAAATCCCCACTTTGAGA  
AGTTCCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATATGAGCGGTTTGTGGTGGCTCCT  
GGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGTGGTGGTCTGCACTCTGGTGTGTC  
CTCTGTGCAGAGCCCCAAGGAAGGTCTGCAGGAGGTCCGGAGAGTACTGAGACCGGGAGGTGTGC  
TCTTTTTCTGGGAGCATGTGGCAGAACCATATGGAAGCTGGGCCTTCATGTGGCAGCAAGTTTTC  
GAGCCCACCTGGAAACACATTGGGGATGGCTGCTGCCTCACCAGAGAGACCTGGAAGGATCTTGA  
GAACGCCCAGTTCTCCGAAATCCAAATGGAACGACAGCCCCCTCCCTTGAAGTGGCTACCTGTTG  
GGCCCCACATCATGGGAAAGGCTGTCAAACAATCTTTCCCAAGCTCCAAGGCACTCATTTGCTCC  
TTCCCCAGCCTCCAATTAGAACAAAGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACCTA  
GCAGAATGAGAGAAGACATTGATGACCACTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGC  
AATCTCTAACTTCAATCCCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGG  
AAACACTAGGACCCCTGTTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCCCTC  
CCAATGTTGTCCCTTTTCCTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACAC  
CCATGCGTCTCTAGGAACTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGAC  
CCTCTCTCCCCACTACCACCTTCTTCTGAGCTGGGGGCACCAGGGAGAATCAGAGATGCTGGGG  
ATGCCAGAGCAAGACTCAAAGAGGCAGAGGTTTTGTTCTCAAATATTTTTTAATAAATAGACGAA  
ACCACG

## **FIGURE 28**

MDILVPLLQLLVLLLTPLPLHLMALLGCWQPLCKSYFPYILMAVLTPKSNRKMESKKRELFSQIKGL  
TGASGKVALLELGCGTGANFQFYPPGCRVTCLDPNPHFEKFLTKSMAENRHLQYERFVVAPGEDM  
RQLADGSMDEVVCTLVLCVQSPRKVLQEVRRVLRPGGVLEFFWEHVAEPYGSWAFMWQQVFPTW  
KHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWLFPVGPIMGKAVKQSFPSKALICSFPSL  
QLEQATHQPIYLPLRGT

**Important features:**

**Signal peptide:**

amino acids 1-23

**Leucine zipper pattern.**

amino acids 10-32

**N-myristoylation sites.**

amino acids 64-70, 78-84, 80-86, 91-97, 201-207



## **FIGURE 29**

CAATGTTTGCCTATCCACCTCCCCAAGCCCCTTTACCTATGCTGCTGCTAACGCTGCTGCTGCT  
GCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGCCAGAAAGTCTCTTCTG  
CCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTCCTTTCTGTGTCTCCTGCCTCAT  
CGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGGAAGGGGAGAAAGTGGGGGATGGCTA  
AGAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGGGGCTGCCTTATTTAAA  
GTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGCCCTGTTTATTAAGAAATT  
GTTCCCTTCCCCTGTGTTCAATGTTTGTAAAGATTGTTCTGTGTAAATATGTCTTTATAATAAAC  
AGTTAAAGCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 30**

MLLLTLLLLLLLLLKGSCLWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHPAMTCSQAQPRG  
EGEKVGDG

**Important features:**

**Signal peptide:**

amino acids 1-15

**Growth factor and cytokines receptors family:**

amino acids 3-18

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### FIGURE 31

GTTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCAAGTT  
CCTCCAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTACTCCCT  
ATTTGCATCTGTTTTGATAAATGATGTTGACACCCTCCACCGAATTCTAAGTGGAAATCATGTCGG  
GAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGTCTTTGGCCATGATGTTTACC  
TTCAGATTCATCACCACCCTTCTGGTTACATTTTCATTTTATTGGTTATTTTGGGATTGTTGTT  
TGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACCTCAGCATAGAATTGGACA  
CAGAAAGGGAAAATATGAAGTGCCTGCTGGGGTTTGCTATCGTATCCACAGGCATCACGGCAGTG  
CTGCTCGTCTTGATTTTTGTTCTCAGAAAGAGAATAAAATTGACAGTTGAGCTTTTCAAATCAC  
AAATAAAGCCATCAGCAGTGCTCCCTTCCTGCTGTTCCAGCCACTGTGGACATTTGCCATCCTCA  
TTTTCTTCTGGGTCTCTGGGTGGCTGTGCTGCTGAGCCTGGGAAGTGCAGGAGCTGCCAGGTT  
ATGGAAGGCGGCCAAGTGAATATAAGCCCCCTTCGGGCATTGGGTACATGTGGTGTGACATTTT  
AATTGGCCTCATCTGGAAGTGAATTCATCCTTGCCTGCCAGCAAATGACTATAGCTGGGGCAG  
TGTTTACTTGTATTTCAACAGAAGTAAAAATGATCCTCCTGATCATCCCATCCTTTCTGCTCTC  
TCCATTCTCTTCTTCTACCATCAAGGAACCGTTGTGAAAGGGTCATTTTTAATCTCTGTGGTGAG  
GATTCCGAGAATCATTGTCTGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCATTGT  
CCAGGTACCTGTTCCGATGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTC  
AACCAGAATGCATATACTACAAGTCTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGC  
ATTCAAATCTTGTCCAAGAACTCAAGTCACTTTACATCTATTAAGTCTTTGGAGACTTCATAA  
TTTTTCTAGGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACTAC  
AATCGGGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTGCCTACTTAGTAGC  
CCATAGTTTTTTATCTGTGTTTGAAACTGTGCTGGATGCACTTTTCTGTGTTTTGCTGTTGATC  
TGGAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTTCGTA  
AAAAGGAGCAACAAATTAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAAGGAATGAGGA  
GGGAACAGAAGTCCAGGCCATTGTGAGATAGATACCCATTTAGGTATCTGTACCTGGAAAACATT  
TCCTTCTAAGAGCCATTTACAGAATAGAAGATGAGACCACTAGAGAAAAGTTAGTGAATTTTTTT  
TAAAAAGACCTAATAAACCCCTATTCTTCCTCAAAA

## **FIGURE 32**

MSGRDTILGLCILALALSLAMMFTFRFITLLVHIFISLVILGLLFVCGVLWWLYDYTDLSIE  
LDTERENMKCVLGFAIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISSAPFLLFQPLWTFA  
ILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFILACQOMTIA  
GAVVTCYFNRSKNPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPIIVMYMQNALKEQQHG  
ALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTAINGTDFCTSAKDAFKILSKNSSHFTSINCFGD  
FIIFLGKVLVVCFTVFGGLMAFNYNRAFQVWAVPLLLVAFFAYLVAHSFLSVFETVLDALFLCFA  
VDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRNEEGTELOAIVR

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **Putative transmembrane domains:**

amino acids 35-54, 75-97, 126-146, 185-204, 333-350, 352-371

#### **N-glycosylation sites.**

amino acids 204-208, 295-299, 313-317

#### **N-myristoylation sites.**

amino acids 147-153, 178-184, 196-202, 296-275, 342-348

Year	1960	1961	1962	1963	1964	1965	1966	1967	1968	1969	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1960	1961	1962	1963	1964	1965	1966	1967	1968	1969	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

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## **FIGURE 34**

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKCPAG  
CQDPKYHVYGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYNGVQSLSLPRWR  
ESFIVLESKPKKGVITYPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQPVTLMQLLAVTVAVA  
TPTTLPRPSPSAASTTIPRPQSVGHRSEQEMDLWSTATYTSSQNRPRADPGIQRQDPSGAAFQKP  
VGADVSLGLVPKEELSTQSLPVS LGDPNCKIDLSFLIDGSTSIGKRRFRIQKQLLADVAQALDI  
GPAGPLMGVVQYGDNPATFHNLTHTNSRDLKTAIEKITQRGGLSNVGRAISFVTKNFFSKANGN  
RSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAENEKQYVVEPNFANKAVCRTNG  
FYSLHVQSWFGLHKTLPVLRVCDTDRLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLQFVTN  
LTKEFEISDTRIGAVQYTYEQRLFGFDKYSSKPDILNAIKRVGYWSGGTSTGAAINFALQQL  
FKKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKGVITYAIGVANAQEELEVIATHPARHSFF  
VDEFDNLHQYVPRIIQNICTEFNSQPRN

### **Important features:**

#### **Signal peptide:**

amino acids 1-26

#### **Transmembrane domain:**

amino acids 181-200

#### **N-glycosylation sites.**

amino acids 390-394, 520-524

#### **N-myristoylation sites.**

amino acids 23-29, 93-99, 115-121, 262-268, 367-373, 389-395,  
431-437, 466-472, 509-515, 570-576, 571-577, 575-581, 627-633

#### **Amidation site.**

amino acids 304-308

## **FIGURE 35**

CCGAGCACAGGAGATTGCCTGCGTTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGAAGAAATTGC  
 CAAACCATGTCTTTTTTCTGTTTTTCAGAGTAGTTCACAACAGATCTGAGTGTTTTAATTAAGCATGGAAT  
 ACAGAAAACAACAAAAAATTAAAGCTTTAATTTTCATCTGGAATTCACAGTTTTCTTAGCTCCCTGGACCC  
 GGTTGACCTGTGGCTCTTCCGCTGGCTGCTCTATCACGTGGTGGCTCTCCGACTACTCACCCCGAGTGTA  
 AAGAACCTTCGGCTCGCGTGCTTCTGAGCTGCTGTGGATGGCCTCGGCTCTCTGGACTGTCCCTCCGAGTA  
 GGATGTCACTGAGATCCCTCAAATGGAGCCTCCTGCTGCTGCTCACTCCTGAGTTTCTTTGTGATGTGGTAC  
 CTCAGCCTTCCCCACTACAATGTGATAGAACGCGTGAAGTGGATGTACTTCTATGAGTATGAGCCGATTTA  
 CAGACAAGACTTTCACCTTCACACTTCGAGAGCATTCAAAGTCTCTCATCAAAATCCATTCTGGTCATTCT  
 TGGTGACCTCCCACCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTACTTGGGGTGAAAAAAGTCT  
 TGGTGGGGATATGAGGTTCTTACATTTTTCTTATTAGGCCAAGAGGCTGAAAAGGAAGACAAAATGTTGGC  
 ATTGTCCTTAGAGGATGAACACCTTCTTTATGGTGACATAATCCGACAAGATTTTTTAGACACATATAATA  
 ACCTGACCTTGAAAACCATATGGCATTAGGTGGGTAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT  
 AAGACAGACACTGATGTTTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTTAAACCTAAACCACTCAGA  
 GAAGTTTTTCACAGGTTATCCTCTAATTGATAATTATTCTATAGAGGATTTTACCAAAAACCCATATTT  
 CTTACCAGGAGTATCCTTTCAAGGTGTTCCCTCCATACTGCAGTGGGTTGGGTTATATAATGTCCAGAGAT  
 TTGGTGCCAAGGATCTATGAAATGATGGGTACGTAAGGATCAAGTTGAAGATGTTTATGTCCGGAT  
 CTGTTTGAATTTATTAAAGTGAACATTCAATTTCCAGAAGACACAAATCTTTTCTTCTATATAGAATCC  
 ATTTGGATGTCTGTCAACTGAGACGTGTGATTGCAGCCCATGGCTTTTCTTCCAAGGAGATCATCACTTTT  
 TGGCAGGTCATGCTAAGGAACACCACATGCCATTATTAAGTTCACATTCTACAAAAGCCTAGAAGGACAG  
 GATACCTTGTGAAAGTGTAAATAAAGTAGGTACTGTGGAAAATTCATGGGGAGGTGAGTGTGCTGGCTT  
 ACACTGAACTGAAACTCATGAAAACCCAGACTGGAGACTGGAGGGTTACACTTGTGATTTATTAGTCAGG  
 CCCTTCAAAGATGATATGTGGAGGAATTAATATATAAGGAATTGGAGGTTTTTGCTAAAGAAATTAATAGG  
 ACCAAACAATTTGGACATGTCATTCTGTAGACTAGAATTTCTTAAAGGGTGTACTGAGTTATAAGCTCA  
 CTAGGCTGTAAAAACAAACAATGTAGAGTTTTATTATTGAACAATGTAGTCACTTGAAGGTTTTGTGTA  
 TATCTTATGTGGATTACCAATTTAAAAATATATGTAGTTCTGTGTCAAAAACTTCTTCACTGAAGTTATA  
 CTGAACAAAATTTTACCTGTTTTTGGTCATTTATAAAGTACTTCAAGATGTTGCAGTATTTTCAGGTTATT  
 ATTATTTAAATTAATTCACTTTGTGTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAAGGATAG  
 TGAATCATCTTTTACATGCAACATTTTCCAGTTACTTAACTGATCAGTTTATTATTGATACATCACTCCA  
 TTAATGTAAAGTCATAGGTCATTATTGCATATCAGTAATCTCTTGGACTTTGTTAAATATTTTACTGTGGT  
 AATATAGAGAAGAATTAAAGCAAGAAAATCTGAAAA

## **FIGURE 36**

MASALWTVLPSRMSLRSLKWSLLLLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPiYRQDFHF  
TLREHSNCSHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQEAEKEDKMLA  
LSLEDEHLLYGDIIRQDFLDTYNNLTTLKTIMAFRWVTEFCPNAKYVMKTDTDVFINTGNLVKYL  
NLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQEYPFKVFPPYCSGLGYIMSRDLVPRIYEMMGHV  
KPIKFEDVYVGICLNLLKVNIPEDTNLFFLYRIHLDVCQLRRVIAAHGFSSKEIITFWQVMLR  
NTTCHY

### **Important features:**

#### **Type II transmembrane domain:**

amino acids 20-39

#### **N-glycosylation sites.**

amino acids 72-76, 154-158, 198-202, 212-216, 326-330

#### **Glycosaminoglycan attachment site.**

amino acids 239-243

#### **Ly-6 / u-PAR domain proteins.**

amino acids 23-37

#### **N-myristoylation site.**

amino acids 271-277



## FIGURE 37

CGCTCGGGCACCAGCCGCGCAAGGATGGAGCTGGGTTGCTGGACCGAGTTGGGGCTCACTTTTCTTCAGCTCCTTCTCATC  
TCGTCCTTGCCAAGAGAGTACACAGTCATTAAATGAAGCCTGCCCTGGAGCAGAGTGGAAATATCATGTGTCGGGAGTGTGTG  
AATATGATCAGATTGAGTGGCTCTGCCCCGAAAGAGGGAAGTCGTGGGTTATACCATCCCTTGCTGCAGGAATGAGGAGAA  
TGAGTGTGACTCCTGCCGTGATCCACCCAGGTTGTACCATCTTTGAAAAGCTGCAAGAGCTGCCGAAATGGCTCATGGGGGGT  
ACCTTGGATGACTTCTATGTGAAGGGTCTACTGTGCAGAGTGGCGAGCAGGCTGGTACGGAGGAGACTGCATGCCATGTG  
GCCAGGTTCTGCGAGCCCCAAAGGGTCAAGTTTGTGGAAAGCTATCCCTAAATGCTCACTGTGAATGGACCATTTCATGC  
TAAACCTGGGTTTGTATCCAACTAAGATTGTGTCATGTTGAGTCTGGAGTTTACTACATGTGCCAGTATGACTATGTTGAG  
GTTCTGATGGAGACAACCGCATGGCCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCCAGCTCCTATCCAGAGCATAG  
GATCCTCACTCCAGCTCCTCTTCCACTCCGATGGCTCCAAGAATTTTACGGTTTCCATGCCATTTATGAGGAGATCACAGC  
ATGCTCCTCATCCCTTGTGTTCCATGACGGCAGTGCCTCTTGACAAGGCTGGATCTTACAAGTGTGCCTGCTGGCAGGC  
TATACTGGGCAGCGCTGTGAAAATCTCCTTGAAGAAAGAAATGCTCAGACCTGGGGGCCAGTCAATGGGTACCAGAAAA  
TAACAGGGGGCCCTGGGCTTATCAACGGAGCGCATGCTAAATTTGGCACCCTGGTGTCTTTCTTTTGTAACTCCTATGT  
TCTTAGTGGCAATGAGAAAAGAACTTGCCAGCAGAAATGGAGAGTGGTCAGGGAACAGCCCATCTGCATAAAAGCCTGCCGA  
GAACCAAAGATTTCAGACCTGCTGAGAAGGAGAGTTCTTCCGATGCAGGTTTCACTCAAGGGAGACACCATTACACAGCTAT  
ACTCAGCGGCCTTCAGCAAGCAGAACTGCAGAGTGGCCCTACCAAGAAGCCAGCCCTTCCCTTTGGAGATCTGCCATGGG  
ATACCAACATCTGCATACCCAGCTCCAGTATGAGTGCATCTCACCTTCTACCGCCGCTGGGCAGCAGCAGGAGGACATGT  
CTGAGGACTGGGAAGTGGAGTGGGCGGGCACCATCTGCATCCCTATCTGCGGGAAAATTGAGAACATCACTGTCTCAAAGA  
CCCCAAGGTTGCGCTGGCGTGGCGTGGCAGGCGCATCTACAGGAGGACCAGCGGGTGCATGACGGCAGCCTACACAAGGAGC  
GTGGTTCTAGTCTGCAGCGGTGCCCTGGTGAATGAGCGCACTGTGGTGGTGGCTGCCCACTGTGTTACTGACCTGGGGAAG  
GTCACCATGATCAAGACAGCAGACCTGAAAGTTGTTTGGGGAAATTTACCGGGATGATGACCGGGATGAGAAGACCATCC  
AGAGCCTACAGATTCTGCTATCATCTGCAATCCCAACTATGACCCCATCTGCTTGTGCTGACATCGCCATCCTGAAGCT  
CCTAGACAAGGCCCGTATCAGCACCCGAGTCCAGCCCATCTGCCTCGCTGCCAGTCGGGATCTCAGCACTTCTTCCAGGAG  
TCCCACATCACTGTGGCTGGCTGGGAATGTCTGGCAGAGCTGAGGAGCCCTGGCTTCAAGAACGACACACTGCGCTCTGGG  
TGGTCAGTGTGGTGGACTCGCTGCTGTGTGAGGAGCAGCATGAGGACCATGGCATCCAGTGAAGTGTCACTGATAACATGTT  
CTGTGCCAGCTGGGAACCCACTGCCCTTCTGATATCTGCACTGCAGAGACAGGAGGCATCGCGGCTGTGCTCTCCCGGA  
CGAGCATCTCTGAGCCACGCTGGCATCTGATGGGACTGGTCAGCTGGAGCTATGATAAAACATGCAGCCACAGGCTCTCCA  
CTGCCCTTACCAGGTTGCTGCCCTTTTAAAGACTGGATTGAAAGAAATATGAAATGAACCATGCTCATGCACTCCTTGAGAAG  
TGTTTCTGTATATCCGTCTGTACGTGTGTCATTGCGTGAAGCAGTGTGGGCCCTGAAGTGTGATTGTCCTGTGAACCTGGCT  
GTGCCAGGGCTTCTGACTTCAGGGACAAAACCTCAGTGAAGGGTGAAGTAGACCTCCATTGCTGGTAGGCTGATGCCGCTCCA  
CTACTAGGACAGCCAATTGGAAGATGCCAGGGCTTGCAGAAGTAAGTTTCTTCAAGAAGACCATATACAAAACCTCTCCA  
CTCCACTGACCTGGTGGTCTTCCCCAATTTTCAATTATACGAATGCCATCAGCTTGACCAGGGAAGATCTGGGCTTCATGAG  
GCCCCTTTGGAGGCTCTCAAGTCTTAGAGAGCTGCTGTGGGACAGCCAGGGCAGCAGAGCTGGGATGTGGTGCATGCCCTT  
TGTGTACATGGCCACAGTACAGTCTGGTCTTTTCTTCCCCATCTTGTACACATTTTAAATAAATAAGGTTGGCTTCT  
GAACCTACAAAAA  
AAAAA

## **FIGURE 38**

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREVVGYT  
IPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDFYVKGIFYCAECRAGWYGGDCMRGQ  
VLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRDGDNRDQII  
KRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSYKC  
ACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTVVSFFCNNSYVLSGNE  
KRTCQONGEWSGKQPICIKACREPKISDLVRRRVLPQVQSRETPLHQLYSAAFSKQKLQSAPTK  
KPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRCLRTGKWSGRAPSCIPICGKIENITAP  
KTQGLRWPWQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNERTVVAAHCVTDLGKVTMIKTADL  
KVVLGKFYRDDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARISTRVQPICLAASR  
DLSTSFQESHITVAGWNVLADVRSPGFKNDTLRSGVSVVDSLLCEEQHEDHGIPVSVTDNMFCA  
SWEPTAPSDICTAETGGIAAVSFPGRASPEPRWHLMGLVSWSYDKTCSHRLSTAFTKVLPFKDWI  
ERNMK

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-23

#### **EGF-like domain cysteine pattern signature.**

amino acids 260-272

#### **N-glycosylation sites.**

amino acids 96-100, 279-283, 316-320, 451-455, 614-618

#### **N-myristoylation sites.**

amino acids 35-41, 97-103, 256-262, 284-290, 298-304, 308-314,  
474-480, 491-497, 638-644, 666-672

#### **Amidation site.**

amino acids 56-60

#### **Serine proteases, trypsin family.**

amino acids 489-506

#### **CUB domain proteins profile.**

amino acids 150-167

## FIGURE 39

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGCCCGTGATTTATTAACGTGGCTTAATC  
TGAAGGTTCTCAGTCAAATTTCTTGTGATCTACTGATTGTGGGGCATGGCAAGGTTTGCTTAAAGGAGCTTGGCTGG  
TTTGGGCCCTTGTAGCTGACAGAAGGTGGCCAGGGAGAATGCAGCACACTGCTCGGAGAATGAAGCGCTTCTGTTGC  
TGGTCTTGCCCTTGGCTCAGTCCTGCTAACTACATTGACAATGTGGGCAACCTGCACTTCCTGTATTTCAGAACTCTGTA  
AAGGTGCCTCCCACTACGGCTGACCAAAGATAGGAAGAGGCGCTCACAAGATGGCTGTCCAGACGGCTGTGCGAGCC  
TCACAGCCACGGCTCCCTCCCAAGAGGTTTCTGCAGCTGCCACCATCTCTTAATGACAGACGAGCTTGGCTTAGACA  
ACCTTGCTTACGTGTCTCGGCAGAGGACGGGCAGCCAGCAATCAGCCAGTGGACTCTGGCCGGAGCAACCGAATA  
GGGCAGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTTAAAAAATAAATCGAGCTTTGAGTGTTCTTCGAA  
GGACAAAGAGCGGGAGTGCAAGTGGCAACCATGCCAGGGCAGGGAAAATTCTGAAAACACCACTGCCCTGAAG  
TCTTTCCAAGGTTGTACCACCTGATTCCAGATGGTGAAATTAACAGCATCAAGATCAATCGAGTAGATCCAGTGAAA  
GCCTCTCTATTAGGCTGGTGGGAGGTAGCGAAACCCCACTGGTCCATATCATTATCCAACACATTTATCGTGATGGGG  
TGATCGCCAGAGACGGCCGGCTACTGCCAGGAGACATCATTTCTAAAGTCAACGGGATGGACATCAGCAATGTCCCTC  
ACAACTACGCTGTGCGTCTCTGCGGCAGCCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTGAACAGAAGTCCGCA  
GCAGGAACAATGGACAGGCCCGGATGCCTACAGACCCCGAGATGACAGCTTTCATGTGATTCTCAACAAAAGTAGCC  
CCGAGGAGCAGCTTGAATAAACTGGTGCAGAGTGGATGAGCCTGGGGTTTTTCATCTCAATGTGCTGGATGGCG  
GTGTGGCATAACGACATGGTCAGCTTGAGGAGAATGACCGTGTGTAGCCATCAATGGACATGATCTTCGATATGGCA  
GCCCAGAAAGTGCGGCTCATCTGATTAGGCCAGTGAAAGACGTGTTACCTCGTGTCCCGCCAGGTTCCGCGAGC  
GGAGCCCTGACATCTTTAGGAAGCCGCTGGAACAGCAATGGCAGCTGGTCCCGAGGCCAGGGGAGAGGAGCAACA  
CTCCCAAGCCCTCCATCCTACAATTACTTGTGATGAGAAGGTGGTAAATATCCAAAAGACCCCGTGAATCTCTCG  
GCATGACCGTCCGAGGGGAGCATCACATAGAGAATGGGATTTGCCTATCTATGTGATCAGTGTTGAGCCCGGAGGAG  
TCATAAGCAGAGATGGAAGAATAAAAACAGGTGACATTTTGTGAATGTGGATGGGGTGAAGTACAGAGGTGAGCC  
GGAGTGAGGCAGTGCCATTATTGAAAAGAACATCATCTCGATAGTACTCAAAGCTTTGGAAGTCAAAGAGTATGAGC  
CCCAGGAAGACTGCAGCAGCCAGCAGCCCTGGACTCCAACCACAACATGGCCCCACCCAGTGACTGCTCCCATCTCT  
GGGTGATGTGGCTGGAATTACCACGGTGCTTGTATACTGTAAAGATATTGTATTACGAAGAACAACAGCTGGAAGTC  
TGGGCTTCTGCATTGTAGGAGGTATGAAGAATACAATGGAAACAAACCTTTTTTCATCAAATCCATTGTTGAAGGAA  
CACCAGCATACAATGATGGAAGAATTAGATGTGGTGATATTCTTCTTGCTGCAATGGTAGAAGTACATCAGGAATGA  
TACATGCTTGCTTGGCAAGACTGCTGAAAGAACTTAAAGGAAGAATTACTCTAACTATTGTTTCTTGGCCTGGCACTT  
TTTTATAGAAATCAATGATGGGTGAGGAGGAAACAGAAAAATCACAATAGGCTAAGAAGTTGAAACACTATATTTATC  
TTGTGAGTTTTTATATTTAAAGAAAGATACATTGTAAAAATGTGAGGAAAGTATGATCATCTAATGAAAGCCAGTT  
ACACCTCAGAAAAATGATTCAAAAAAATTAATACTACTAGTTTTTTTTCAGTGTGGAGGATTTCTCATTACTCTAC  
AACATTGTTTATATTTTTCTATTCAATAAAAGCCCTAAACAACATAAATGATTGATTTGTATACCCCACTGAATT  
CAAGCTGATTTAAATTTAAATTTGGTATATGCTGAAGTCTGCCAAGGTACATTATGGCCATTTTAAATTTACAGCT  
AAAAATTTTTTAAATGCATTGCTGAGAACGTTGCTTTTCATCAACAAGAATAAATTTTTTCAGAAGTTAAA

## **FIGURE 40**

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPCDGCASLTATAPS  
PEVSAAATISLMTDEPGLDNPAYVSSAEDGQPAISPVDSGRSNRTRARPFERSTIRSRSFKKINR  
ALSVLRRTKSGSAVANHADQGRESENTTAPEVFPRLYHLIPDGEITSIKINRVDPSESLSIRLV  
GGSETPLVHIIIQHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLLRQPCQVLWLTVM  
REQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIKLVRKVDEPGVFIFNVLDGGVAYRHG  
QLEENDRVLAINGHDLRYGSPESAHLIQASERRVHLVVSQRQRSPDIFQEAGWNSNGSWSPG  
PGRSNTPKPLHPTITCHEKVNIQKDPGESLGMTVAGGASHREWDLPIYVISVEPGGVISRDGR  
IKTGDILLNVVGVELTEVSRSEAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNHNMAP  
SDWSPSWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIVGGYEEYNGNKPFFIKSIVEGTPAYNDG  
RIRCGDILLAVNGRSTSGMIHACLARLLKELKGRITLTIVSWPGTFL

### **Important features:**

#### **Signal peptide:**

amino acids 1-15

#### **N-glycosylation sites.**

amino acids 108-112, 157-161, 289-293, 384-388

#### **Tyrosine kinase phosphorylation sites.**

amino acids 433-441, 492-500

#### **N-myristoylation sites.**

amino acids 51-57, 141-147, 233-239, 344-350, 423-429, 447-453,  
467-473, 603-609

## FIGURE 41

ACCAGGCATTGTATCTTCAGTTGTCATCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGAAGCTTT  
CTTGCCCTGCAGTGAAGCAGAGAGATAGATATTATTACGTAATAAAAAACATGGGCTTCAACCTGACT  
TTCCACCTTTCTACAAATCCGATTACTGTTGCTGTTGACTTTGTGCTGACAGTGGTTGGGTGGGC  
CACCAGTAACTACTTCGTGGGTGCCATTCAAGAGATTCTAAAGCAAAGGAGTTCATGGCTAATTTCC  
ATAAGACCTCATTTTGGGAAGGGAAAACTCTGACTAATGAAGCATCCACGAAGAAGGTAGAACTT  
GACAACGTCTCTTCTGTGTCTCTTACCTCAGAGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCAC  
TTTGAAGAGGTACAGGCAGAAAATCCCAAAGTGTCCAGAGGCCGGTATCGCCCTCAGGAATGTAAAG  
CTTTACAGAGGGTGCCTATCCTCGTTCCCCACCGGAACAGAGAGAAACACCTGATGTACCTGCTGGAA  
CATCTGCATCCCTTCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCACCAGGCTGAAGG  
TAAAAAGTTAATCGAGCCAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAATTGGG  
ACTGCTTTATATTCCACGATGTGGACCTGGTACCGAGAATGACTTTAACCTTTACAAGTGTGAGGAG  
CATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTGGATATTTGG  
GGGTGTTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCTAACAACTACTGGGGAT  
GGGGAGGCGAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAAGAATGAAAATTTCCCGCCCCCTG  
CCTGAAGTGGGTAAATATACAATGGTCTTCCACACTAGAGACAAAGGCAATGAGGTGAACGCAGAACG  
GATGAAGCTCTTACACCAAGTGTACGAGTCTGGAGAACAGATGGGTTGAGTAGTTGTTCTTATAAAT  
TAGTATCTGTGGAACACAATCCTTTATATATCAACATCACAGTGGATTTCTGGTTTGGTGCATGACCC  
TGGATCTTTTGGTGATGTTTGAAGAAGTATTCTTTGTTTGAATAATTTTGGCCTAGAGACTTCAA  
ATAGTAGCACACATTAAGAACCTGTACAGCTCATTGTTGAGCTGAATTTTCTTTTGTATTTCT  
TAGCAGAGCTCCTGGTGATGTAGAGTATAAAACAGTTGTAACAAGACAGCTTCTTAGTCATTTTGAT  
CATGAGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGATAA  
AATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTATTTAAATTTGAAGTAATATATTATGGGAT  
AAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCTCGTCCAAGGTAGAA  
AGGTACGAAGATACAATACTGTTATTCAATTATCCTGTACAATCATCTGTGAAGTGGTGGTGCAGGT  
GAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCGACGAATCAGGACACAGTGAAGTGGGAATGAAGA  
GGTAGCAGGAGGGTGGAGTGTGCGCTGCAAAGGCAGCAGTAGCTGAGCTGGTTGCAGGTGCTGATAGC  
CTTCAGGGGAGGACCTGCCAGGTATGCCCTTCAGTGATGCCACCAGAGAATACATTCTCTATTAGT  
TTTTAAAGAGTTTTTGTAAAATGATTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACAT  
ATTAACATAATAAATATGTCTATCAAATACCTCTGTAGTAAAATGTGAAAAAGCAAAA

## **FIGURE 42**

MGFNLT FHLSYKFRLLLLLTLCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLILGKGKTLTN  
EASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYPQECKALQRVAILVPH  
RNREKHLMYLLEHLHPFLQRQQLDYGIIYVIHQAEKGKFNRAKLLNVGYLEALKEENWDCFI FHDV  
DLVPENDFNLYKCEEHPKHLVVGRNSTGYRLRYSGYFGGVLTALSREQFFKVNGFSNNYWGWGGE  
DDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSRVWRTDGLSSCSYKLV  
SVEHNPLYINITVDFWFGA

**Important features:**

**Signal peptide:**

amino acids 1-27

**N-glycosylation sites.**

amino acids 4-8, 220-224, 335-339

**Xylose isomerase proteins.**

amino acids 191-202

### **FIGURE 43**

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACGATGGCACTGAGCTCCCAGATCTGGG  
CCGCTTGCCTCCTGCTCCTCCTCCTCGCCAGCCTGACCAGTGGCTCTGTTTTCCCACAACAG  
ACGGGACAACCTGCAGAGCTGCAACCCAGGACAGAGCTGGAGCCAGGGCCAGCTGGATGCCCAT  
GTTCCAGAGGCGAAGGAGGCGAGACACCCACTTCCCCATCTGCATTTTCTGCTGCGGCTGCTGTC  
ATCGATCAAAGTGTGGGATGTGCTGCAAGACGTAGAACCTACCTGCCCTGCCCCGTCCCCTCCC  
TTCCTTATTTATTCTGCTGCCCCAGAACATAGGTCTTGAATAAAATGGCTGGTTCTTTTGT  
TCCAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 44**

MALSSQIWAACLLLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRDTHFPI  
CIFCCGCCCHRSKCGMCCKT

Important features:

Signal peptide:

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 58-59

N-myristoylation site.

amino acids 44-50

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 1-12



## FIGURE 45

GTGGCTTCATTTCAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCCAACATGCCTCACCC  
TCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTGGTCGGT  
TCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTCTATTGTCTG  
GACCTTCAACACAACCCCTCTTGTACCATAACAGCCAGAAGGGGGCACTATCATAGTGACCCAAA  
ATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAGCTCAGCAAAGTGAAG  
AAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCA  
GGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCA  
ATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATT  
TATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTCCCATAATGGGTCCATCCTCCCCATCTC  
CTGGAGATGGGGAGAAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCCTGTGAGCAGAACT  
TCTCAAGCCCCATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCCATG  
GTCCTCCTGTGTCTCCTGTTGGTGCCCCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTG  
GTTTCTGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTCGGG  
AAACTCCTAACATATGCCCCCATTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAAT  
AGAACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAAAGAT  
GGAAAAATCCCCACTCACTGCTCACGATGCCAGACACACCAAGGCTATTTGCCTATGAGAATGTTA  
TCTAGACAGCAGTGCCTCCCCCTAAGTCTCTGCTCA

## **FIGURE 46**

MAGSPTCLTLIYILWQLTGSAAAGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVTIQP  
EGGTIIIVTQNRNRERVDFFDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHVYEHLSK  
PKVTMGLQSNKNGTCVTNLTCMEHGEEVDVIYTWKALGOANESHNGSILPISWRWGESDMTFIC  
VARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSLFLVLGLFLWFLKRERQEEYIE  
EKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPANTVYSTVEIPKKMENPHSLLTMPDT  
PRLFAYENVI

### **Important features:**

#### **Signal peptide:**

amino acids 1-22

#### **Transmembrane domain:**

amino acids 224-250

#### **Leucine zipper pattern.**

amino acids 229-251

#### **N-glycosylation sites.**

amino acids 98-102, 142-146, 148-152, 172-176, 176-180, 204-208,  
291-295

## **FIGURE 47**

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAATGG  
ATTCAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTGTCAGCT  
TAGTTGAGGAAGACCAATTTCTCAAACCCCATCTCTTGCTTTGAGTGGTGGTCCCAGGAATT  
ATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAGAAAAAGAGCGTG  
CTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTTCAGTGTGATCACAGTCATTGGTGCTC  
TGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTCATGTGTAATTCTCCAAGC  
AACAGTAATGCCAATTGTGAATTTTCATTGAAAACATCAGTGACATTCATCCAGAATCCTTCAA  
CTTGCAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTGGTTTCAATAAACCCACCAGTAACG  
ACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCACTTCGATTCTGAAGAAAACAAACATAGG  
CTTATCCACTTCTCAGTATTTTtaggtctattgcttggttgaattctggaggtcctgtttgggct  
CAGTCAGATAGTCATCGGTTTCCTTGGCTGTCTGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTG  
TGTAGTTTAAATGGGAATAAAATGTAAGTATCAGTAGTTTGAAAAAAAAAA

## **FIGURE 48**

MTCCEGWTS CNGFSL LVL LLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMAIPA  
TTMSLTARKRACCNRTGMFLSSFFSVITVIGALYCLISIQALLKGPLMCNSPSNSNANCEFSL  
KNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSSEENKHRLIHFSVFLGL  
LLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

### **Important features:**

#### **Transmembrane domains:**

amino acids 10-31 (type II), 50-72, 87-110, 191-213

#### **N-glycosylation sites.**

amino acids 80-84, 132-136, 148-152, 163-167

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 223-227

#### **N-myristoylation sites.**

amino acids 22-28, 54-60, 83-89, 97-103, 216-222

#### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 207-218

#### **TNFR/NGFR family cysteine-rich region protein.**

amino acids 4-12

## FIGURE 49

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGGTGA  
AGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTGGAGCAG  
ATCCGTGGGCTGCAGACCCCGCCCCAGTGCTCTCCCCCTGCAGCCCTGCCCCCTCGAACTGTGA  
CATGGGAGAGAGTGACCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGGAAGCCAATGACC  
CATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAGCTGAGCGGACTGATC  
TGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGGCAAATGCAAATACAAGAG  
CAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCACTCATCACTCCAGGCTCTGCCA  
CTACTTGCTTGAGCACAGGACTGGCCTCCAGGGATGGCCTGAAGCCTAACACTGGCCCCCAGCACC  
TCCTCCCCCTGGGAGGCCCTTATCCTCAAGGAAGGACTTCTCTCCAAGGCAGGCTGTTAGGCCCT  
TTCTGATCAGGAGGCTTCTTTATGAATTAAACTCGCCCCACCACCCCTCA

## **FIGURE 50**

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAAGIAAVLSGKCKYKS  
SQKQHSPVPEKAIPILITPGSATTC

**Important features:**

**Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 36-59

**N-myristoylation sites.**

amino acids 41-47, 45-51, 84-90

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7.**

amino acids 54-67

## FIGURE 51

GTGGACTCTGAGAAGCCCAGGCAGTTGAGGACAGGAGAGAGAAGGCTGCAGACCCAGAGGGAGGG  
AGGACAGGGAGTCGGAAGGAGGAGGACAGAGGAGGGCACAGAGACGCAGAGCAAGGGCGGCAAGG  
AGGAGACCCTGGTGGGAGGAAGACACTCTGGAGAGAGAGGGGGCTGGGCAGAGATGAAGTTCCAG  
GGGCCCCCTGGCCTGCCTCCTGCTGGCCCTCTGCCTGGGCAGTGGGGAGGCTGGCCCCCTGCAGAG  
CGGAGAGGAAAGCACTGGGACAAATATTGGGGAGGCCCTTGGACATGGCCTGGGAGACGCCCTGA  
GCGAAGGGGTGGGAAAGGCCATTGGCAAAGAGGCCGGAGGGGCAGCTGGCTCTAAAGTCAGTGAG  
GCCCTTGGCCAAGGGACCAGAGAAGCAGTTGGCACTGGAGTCAGGCAGGTTCCAGGCTTTGGCGC  
AGCAGATGCTTTGGGCAACAGGGTCGGGGAAGCAGCCCATGCTCTGGGAAACACTGGGCACGAGA  
TTGGCAGACAGGCAGAAGATGTCATTCGACACGGAGCAGATGCTGTCCGCGGCTCCTGGCAGGGG  
GTGCCTGGCCACAGTGGTGCTTGGGAACTTCTGGAGGCCATGGCATCTTTGGCTCTCAAGGTGG  
CCTTGGAGGCCAGGGCCAGGGCAATCCTGGAGGTCTGGGACTCCGTGGGTCCACGGATACCCCCG  
GAAACTCAGCAGGCAGCTTTGGAATGAATCCTCAGGGAGCTCCCTGGGGTCAAGGAGGCAATGGA  
GGGCCACCAAACCTTTGGGACCAACACTCAGGGAGCTGTGGCCCAGCCTGGCTATGGTTCAGTGAG  
AGCCAGCAACCAGAATGAAGGGTGACGAATCCCCCACCATCTGGCTCAGGTGGAGGCTCCAGCA  
ACTCTGGGGGAGGCAGCGGCTCACAGTCGGGCAGCAGTGGCAGTGGCAGCAATGGTGACAACAAC  
AATGGCAGCAGCAGTGGTGGCAGCAGCAGTGGCAGCAGCAGTGGCAGCAGCAGTGGCGGCAGCAG  
TGGCGGCAGCAGTGGTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGCAGTGAGT  
CCTCCTGGGGATCCAGCACCGGCTCCTCCTCCGGCAACCACGGTGGGAGCGGCGGAGGAAATGGA  
CATAAACCCGGGTGTGAAAAGCCAGGGAATGAAGCCCGCGGGAGCGGGGAATCTGGGATTCAGGG  
CTTCAGAGGACAGGGAGTTTCCAGCAACATGAGGGAAATAAGCAAAGAGGGCAATCGCCTCCTTG  
GAGGCTCTGGAGACAATTATCGGGGGCAAGGGTCGAGCTGGGGCAGTGGAGGAGGTGACGCTGTT  
GGTGGAGTCAATACTGTGAACTCTGAGACGTCTCCTGGGATGTTTAACTTTGACACTTTCTGGAA  
GAATTTTAAATCCAAGCTGGGTTTCATCAACTGGGATGCCATAAACAAGGACCAGAGAAGCTCTC  
GCATCCCGTGAACCTCCAGACAAGGAGCCACCAGATTGGATGGGAGCCCCCAGCTCCCTCCTTAA  
AACACCACCCTCTCATCTAATCTCAGCCCTTGCCCTTGAAATAAACCTTAGCTGCCCCACAAA  
AA  
AA

Year	1950	1951	1952	1953	1954	1955	1956	1957	1958	1959	1960	1961	1962	1963	1964	1965	1966	1967	1968	1969	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1950	1951	1952	1953	1954	1955	1956	1957	1958	1959	1960	1961	1962	1963	1964	1965	1966	1967	1968	1969	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

Signal peptide:

N-glycosylation site.

Glycosaminoglycan attachment site.

Casein kinase II phosphorylation site.

N-myristoylation site.

Cell attachment sequence.

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## FIGURE 53

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGGATGTCGCTGCTGAGCCTGCCCTGG  
CTGGGCCTCAGACCGGTGGCAATGTCCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTCCTGGCT  
ACTCGCCCGCATCCTGGCTTGACCTATGCCTTCTATAACAACCTGCCGCCGGCTCCAGTGTTC  
CACAGCCCCAAAACGGAACGGTTTTTGGGGTCACCTGGGCCTGATCACTCCTACAGAGGAGGGC  
TTGAAGGACTCGACCCAGATGTCGGCCACCTATTCCCAGGGCTTTACGGTATGGCTGGGTCCCAT  
CATCCCCCTTCATCGTTTTATGCCACCCTGACACCATCCGGTCTATACCAATGCCCTCAGCTGCCA  
TTGCACCCAAGGATAATCTCTTCATCAGGTTCTGAAGCCCTGGCTGGGAGAAGGGATACTGCTG  
AGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGACGCCCGCCTTCATTTC AACATCCT  
GAAGTCTATATAACGATCTTCAACAAGAGTGCAAACATCATGCTTGACAAGTGGCAGCACCTGG  
CCTCAGAGGGCAGCAGTCGTCTGGACATGTTTGAGCACATCAGCCTCATGACCTTGACAGTCTA  
CAGAAATGCATCTTCAGCTTTGACAGCCATTGTGAGGAGAGGCCAGTGAATATATTGCCACCAT  
CTTGAGACTCAGTGCCCTTGTAGAGAAAAGAAGCCAGCATATCCTCCAGCACATGGACTTTCTGT  
ATTACCTCTCCCATGACGGGCGGCGCTTCCACAGGGCCTGCCGCTGGTGCATGACTTCACAGAC  
GCTGTCATCCGGGAGCGGCGTCGCACCTCCCCACTCAGGGTATTGATGATTTTTTCAAAGACAA  
AGCCAAGTCCAAGACTTTGGATTTTATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGG  
CATTGTGATGAGGATATAAGAGCAGAGGCTGACACCTTCATGTTTGAGGCCATGACACCACG  
GCCAGTGGCCTCTCCTGGGTCTGTACAACCTTGCGAGGCACCCAGAATACCAGGAGCGCTGCCG  
ACAGGAGGTGCAAGAGCTTCTGAAGGACCGGATCCTAAAGAGATTGAATGGGACGACCTGGCCC  
AGCTGCCCTTCTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCAGCTCCCTTCATC  
TCCCGATGCTGCACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTG  
CCTCATCGATATTATAGGGGTCCATCACAACCCAACTGTGTGGCCGGATCCTGAGGTCTACGACC  
CCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTACCTCTGGCTTTTATTCCCTTCTCCGCA  
GGGCCCAGGAAGTGCATCGGGCAGGCGTTGCCATGGCGGAGATGAAAGTGGTCCCTGGCGTTGAT  
GCTGCTGCACTTCCGGTTCTGCCAGACCACACTGAGCCCCGAGGAAGCTGGAATTGATCATGC  
GCCCGAGGGCGGGCTTTGGCTGCGGGTGAGCCCCCTGAATGTAGGCTTGCACTGACTTTCTGAC  
CCATCCACCTGTTTTTTTGCAGATTGTCATGAATAAACGGTGCTGTCAA

## **FIGURE 54**

MSLLSLPWLGLRPVAMSPWLLLLLVGSWLLARILAWTYAFYNNCRRLQCFPPKRNWFWGHLG  
LITPTEEGLKDSTQMSATYSQGFTVWLGPPIPFIVLCHPDTIRSITNASAAIAPKDNLFIRFLKP  
WLGEIGILLSSGDKWSRHRMLTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGSSRLDMFEHI  
SLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYYLSHDGRRFHRAC  
RLVHDFTDVIRERRRTLPTQGIDDFKDKAKSKTLDFIDVLLLSKDEDGKALSDEDIRAEADTF  
MFGGHDTTASGLSWVLYNLARHPEYQERCQEVQELLKDRDPKEIEWDDLAQLPFLTMCVKESLR  
LHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVWPDPEVYDPFRFDPENSKGRSP  
LAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHTEPRRKLELIMRAEGGLWLRVEPLN  
VGLQ

### **Important features:**

#### **Transmembrane domains:**

amino acids 13-32 (type II), 77-102

#### **Cytochrome P450 cysteine heme-iron ligand signature.**

amino acids 461-471

#### **N-glycosylation sites.**

amino acids 112-116, 168-172

## FIGURE 55

ATCGCATCAATTGGGAGTACCATCTTCCTCATGGGACCAGTGAAACAGCTGAAGCGAATGTTTGA  
GCCTACTCGTTTGATTGCAACTATCATGGTGCTGTTGTGTTTTGCACTTACCCTGTGTTCTGCCT  
TTGGTGGCATAACAAGGGACTTGCACTTATCTTCTGCATTTTGCAGTCTTTGGCATTGACGTGG  
TACAGCCTTTCCTTCATACCATTGCAAGGGATGCTGTGAAGAAGTGTTTTGCCGTGTGTCCTGC  
ATAATTTCATGGCCAGTTTTATGAAGCTTTGGAAGGCACTATGGACAGAAGCTGGTGGACAGTTTT  
GTAACATCTTCGAAACCTCTGTCTTACAGACATGTGCCTTTTATCTTGCAGCAATGTGTTGCCT  
GTGATTCGAACATTTGAGGGTTACTTTTGAAGCAACAATACATTCTCGAACCTGAATGTCAGTA  
GCACAGGATGAGAAGTGGGTTCGTATCTTGTGGAGTGGAACTTCCTCATGTACCTGTTTCCTC  
TCTGGATGTTGTCCCACTGAATCCCATGAATACAAACCTATTTCAGCAACAGCAAAAAAAAAAAAA  
AA

## **FIGURE 56**

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSFIPFAR  
DAVKKCFVCLA

**Important features:**

**Signal peptide:**

amino acids 1-33

**Type II fibronectin collagen-binding domain protein.**

amino acids 30-72

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## FIGURE 57

CGGCTCGAGCTCGAGCCGAATCGGCTCGAGGGGCACTGGAGCACCCAGCAGGCCGCCAATGCTCTGTCTGTGCCTG  
TACGTGCCGGTTCATCGGGGAAGCCAGACCGAGTTCCAGTACTTTGAGTCGAAGGGGCTCCCTGCCGAGCTGAAGTCC  
ATTTTCAAGCTCAGTGTCTTCATCCCCCTCCAGGAATTTCACCTACCGCCAGTGGAGCAGAAAAATTGTACAAGCT  
GGAGATAAGGACCTTGATGGGCAGCTAGACTTTGAAGAATTTGTCCATTATCTCCAAGATCATGAGAAGAAGCTGAGG  
CTGGTGTTTAAGATTTTGGACAAAAGAATGATGGACGCATTGACGCGCAGGAGATCATGCAGTCCCTGCCGGACTTG  
GGAGTCAAGATATCTGAACAGCAGGCAGAAAAAATTCAGAGCATGGATAAAAACGGCAGCATGACCATCGACTGG  
AACGAGTGGAGAGACTACCACCTCTCCACCCCGTGGAAAACATCCCGAGATCATCCTCTACTGGAAGCATTCCACG  
ATCTTTGATGTGGGTGAGAATCTAACGGTCCCGGATGAGTTACAGTGGAGGAGAGGACAGCGGGGATGTGGTGGAGA  
CACCTGGTGGCAGGAGGTGGGGCAGGGGCCGTATCCAGAACCTGCACGGCCCCCTGGACAGGCTCAAGGTGCTCATG  
CAGGTCCATGCCCTCCCGCAGCAACAACATGGGCATCGTTGGTGGCTTCACTCAGATGATTGAGAAGGAGGGGCCAGG  
TCACTCTGGCGGGCAATGGCATCAACGTCTCAAAATTGCCCGCAATCAGCCATCAAATTCATGGCCTATGAGCAG  
ATCAAGCGCTTGTGGTAGTGACAGGAGACTCTGAGGATTCACGAGAGGCTTGTGGCAGGGTCCCTGGCAGGGGCC  
ATCGCCAGAGCAGCATCTACCCAATGGAGGTCCCTGAAGACCCGGATGGCGCTCGCGAAGACAGGGCCAGTACTCAGGA  
ATGCTGGACTGCCCGAGGAGGATCCTGGCCAGAGAGGGGGTGGCCGCTTCTACAAAGGCTATGTCCCCAACATGCTG  
GGCATCATCCCCATGCCGGCATCGACCTTGCACTACGAGAGCGCTCAAGAATGCCTGGCTGCAGCACTATGCAGTG  
AACAGCGCGGACCCCGGCTGTTGTGTCTCTGGCCTGTGGCACCATGTCCAGTACCTGTGGCCAGCTGGCCAGCTAC  
CCCCCTGGCCCTAGTCAGGACCCGGATGCAGGCGCAAGCCTCTATTGAGGGCGCTCCGGAGGTGACCATGAGCAGCCTC  
TTCAACATATCCTGCGGACCGAGGGGGCCTTCGGGCTGTACAGGGGGCTGGCCCCAACTTCATGAAGGTCAATCCCA  
GCTGTGAGCATCAGTACGTGCTCTACAGAACTGAAGATCACCTGGGCGTGCAGTCCGGTGAAGGGGGAGGGC  
CGCCCGGAGTGGACTCGCTGATCCTGGGCGCAGCCTGGGGTGTGCAGCCATCTCATTCTGTGAATGTGCCAACACT  
AAGCTGTCTCGAGCCCAAGCTGTGAAAACCTAGACGCACCCGAGGGAGGGTGGGGAGAGCTGGCAGGCCAGGGCTT  
GTCTGTGACCCAGCAGACCTCTCTGTTGGTTCACGCAAGACCACAGGCATTCTTAGGGTCCAGGGTCAGCAGG  
CTCCGGGCTCAGATGTGAAGGACAGGACATTTCTGCAGTGCCTGCCAATAGTGAGCTTGGAGCCTGGAGGCCGGCT  
TAGTTCTTCCATTTACCCCTTGACGCCAGCTGTTGGCCACGGCCCCCTGCCCTCTGGTCTGCCGTGCATCTCCCTGTGC  
CCTCTGTGCTGCCGTGTCTGCTGAGGTAAAGTGGGAGGAGGGCTACAGCCACATCCCACCCCTCGTCCAATCCC  
ATAATCCATGATGAAAGGTGAGGTACGTGGCCTCCAGGCCCTGACTTCCCAACCTACAGCATTGACGCCAACTTGGC  
TGTGAAGGAAGAGGAAAGGATCTGGCCTTGTGGTCACTGGCATCTGAGCCCTGCTGATGGCTGGGGCTCTCGGGCATG  
CTTGGGAGTGCAGGGGGCTCGGGCTGCCTGGCCTGGCTGCACAGAAGGCAAGTGTGGGGCTCATGGTGTCTGAGCT  
GGCCTGGACCCTGTGAGGATGGGGCCACCTCAGAACCAACTCACTGTCCCCACTGTGGCATGAGGGCAGTGGAGCA  
CCATGTTTGAAGGCGAAGGGCAGAGCGTTTGTGTGTTCTGGGGAGGGAAGGAAAGGTGTTGGAGGCCCTTAATTATGG  
ACTGTTGGGAAAGGGTTTTGTCCAGAAGGACAAGCCGGACAAATGAGCGACTTCTGTGCTTCCAGAGGAAGACGAGG  
GAGCAGGAGCTTGGCTGACTGCTCAGAGTCTGTTCTGACGCCCTGGGGGTCTCTGTCCAACCCAGCAGGGGCGCAGC  
GGGACCAGCCCCACATTCCACTTGTGTCACTGCTTGGAACTATTTATTTGTATTTATTTGAACAGAGTTATGTCT  
AACTATTTTATAGATTTGTTTAATTAATAGCTTGTCAATTTCAAGTTCAATTTTATTCATATTTATGTTATGTTG  
GATTGTACCTTCCCAAGCCCCCAGTGGGATGGGAGGAGGAGGAGAGGGGGGCTTGGGGCGCTGCAGTCACATCT  
GTCCAGAGAAATTCCTTTTGGGACTGGAGGCAGAAAGCGGCCAGAGGCAGCAGCCCTGGCTCCTTTCTTTTGGCAG  
GTTGGGGAAGGGCTTGCCCCAGCCTTAGGATTTAGGGTTTGAAGTGGGGCGTGGAGAGAGGGGAGGAACCTCAAT  
AACCTTGAAGGTGGAATCCAGTTATTTCTGCGCTGCGAGGGTTCTTTATTTCACTCTTTTCTGAATGTCAAGGCAG  
TGAGGTGCTCTCACTGTGAATTTGTGGTGGGCGGGGGCTGGAGGAGAGGGTGGGGGCTGGCTCCGTCCCTCCCAGC  
CTTCTGCTGCCCTTGCTTAACAATGCCGGCCAACTGGCGACCTCACGTTGCACTTCCATTCCACCAGAATGACCTGA  
TGAGGAATCTTCAATAGGATGCAAGATCAATGCAAAAATGTTATATATGAACATATACTGGAGTCGTCAAAAAG  
CAAAATTAAGAAAGAAATTGGACGTTAGAAGTTGTCAATTAAGCAGCCTTCAATAAAGTTGTTTCAAGCTGAAAAA  
AA

## **FIGURE 58**

MLCLCLYVPVIGEAQTEFQYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKDLDG  
QLDFEEFVHYLQDHEKKLRILVFKILDKNDGRIDAQEI MQSLRDLGVKISEQQAEKILKSMDKNG  
TMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTVEERQTGMWWRHLVAGGG  
AGAVSRTCTAPLDRCLKVLMQVHASRSNNMGIVGGFTQMIREGGARSLWRGNGINVLKIAPESAIG  
FMAYEQIKRLVGSDQETLRIHERLVAGSLAGAIQSSIYPMEVLKTRMALRKTGQYSGMLDCARR  
ILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNWLQHYAVNSADPGVFVLLACGTMSSTC  
GQLASYPLALVRTRMQAASIEGAPEVTMSSLFKHILRTEGAFGLYRGLAPNFMKVIPAVSISYV  
VYENLKITLGVQSR

### **Important features:**

#### **Signal peptide:**

amino acids 1-16

#### **Putative transmembrane domains:**

amino acids 284-304, 339-360, 376-394

#### **Mitochondrial energy transfer proteins signature.**

amino acids 206-215, 300-309

#### **N-glycosylation sites.**

amino acids 129-133, 169-173

#### **Elongation Factor-hand calcium-binding protein.**

amino acids 54-73, 85-104, 121-140

## FIGURE 59

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCCATGGC  
TTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAGCAATTG  
CACTCATCATTGGCTTTTGGTATTTTCAGGGAGACACTCCATCACAGTCACTACTGTCGCCTCAGCT  
GGGAACATTGGGGAGGATGGAATCCTGAGCTGCACCTTTGAACCTGACATCAAACCTTTCTGATAT  
CGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCAAAGAAGGCAAAGATG  
AGCTGTGCGAGCAGGATGAAATGTTTCAGAGGCCGGACAGCAGTGTTCGCTGATCAAGTGATAGTT  
GGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGCTGGCACCTACAAATGTTATAT  
CATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATAAACTGGAGCCTTCAGCATGCCGG  
AAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTGCGGTGTGAGGCTCCCCGATGGTTCCCC  
CAGCCCACAGTGGTCTGGGCATCCCAAGTTGACCAGGGAGCCAACCTTCTCGGAAGTCTCCAATAC  
CAGCTTTGAGCTGAACTCTGAGAATGTGACCATGAAGGTTGTGTCTGTGCTCTACAATGTTACGA  
TCAACAACACATACTCCTGTATGATTGAAAAATGACATTGCCAAAGCAACAGGGGATATCAAAGTG  
ACAGAATCGGAGATCAAAGGCGGAGTCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTGTGT  
CTCTTCTTTCTTTGCCATCAGCTGGGCACCTTCTGCCTCTCAGCCCTTACCTGATGCTAAAATAAT  
GTGCCTTGGCCACAAAAAGCATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTTTAC  
CACCAGATATGACCTAGTTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTG  
AGCAAACAAGAGCAAGAAACAAAAAGAAGCCAAAGCAGAAGGCTCCAATATGAACAAGATAAAT  
CTATCTTCAAAGACATATTAGAAGTTGGGAAAATAATTCATGTGAACTAGACAAGTGTGTTAAGA  
GTGATAAGTAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGT  
CACCTGGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTATGTTATATGTGC  
TGTAATGTTGCTCTGAGGAAGCCCCCTGGAAAGTCTATCCCAACATATCCACATCTTATATCCAC  
AAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGGGGCG  
GCTGCATTTTATGTAATGGGTCAAATGATTCACTTTTTATGATGCTTCCAAAGGTGCCTTGGCTTC  
TCTTCCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAAACAGAGCAGT  
CGGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTAAACAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 6o**

MASLGQILFWSIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDIKLS  
DIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKNVQLTDAGTYKC  
YIITSKGKGNANLEYKTGAFSMPEVNVVDYNASSETLRCEAPRWFPQPTVVWASQVDQGANFSEVS  
NTSFELNSENVTMKVVSVLYNVTINNTYSCMIENDIAKATGDIKVTSEIKRRSHLQLLNSKASL  
CVSSFFAISWALLPLSPYMLK

### **Important features:**

#### **Signal peptide:**

amino acids 1-28

#### **Transmembrane domain:**

amino acids 258-281

#### **N-glycosylation sites.**

amino acids 112-116, 160-164, 190-194, 196-200, 205-209, 216-220,  
220-224

#### **N-myristoylation sites.**

amino acids 52-58, 126-132, 188-194



## FIGURE 61

TGACGTCAGAATCACCATGGCCAGCTATCCTTACCGGCAGGGCTGCCAGGAGCTGCAGGACAAG  
CACCAGGAGCCCCCTCCGGGTAGCTACTACCCTGGACCCCCCAATAGTGGAGGGCAGTATGGTAGT  
GGGCTACCCCTGGTGGTGGTTATGGGGGTCTGCCCTGGAGGGCCTTATGGACCACCAGCTGG  
TGGAGGGCCCTATGGACACCCCAATCCTGGGATGTTCCCTCTGGAACCTCAGGAGGACCATATG  
GCGGTGCAGCTCCCGGGGGCCCCCTATGGTCAGCCACCTCCAAGTTCTACGGTGCCAGCAGCCT  
GGGCTTTATGGACAGGGTGGCGCCCCCTCCAATGTGGATCCTGAGGCCTACTCCTGGTTCCAGTC  
GGTGGACTCAGATCACAGTGGCTATATCTCCATGAAGGAGCTAAAGCAGGCCCTGGTCAACTGCA  
ATTGGTCTTCATTCAATGATGAGACCTGCCTCATGATGATAAACATGTTTGACAAGACCAAGTCA  
GGCCGCATCGATGTCTACGGCTTCTCAGCCCTGTGGAAATTCATCCAGCAGTGAAGAACCTCTT  
CCAGCAGTATGACCGGGACCGCTCGGGCTCCATTAGCTACACAGAGCTGCAGCAAGCTCTGTCCC  
AAATGGGCTACAACCTGAGCCCCCAGTTCACCCAGCTTCTGGTCTCCCGCTACTGCCACGCTCT  
GCCAATCCTGCCATGCAGCTTGACCGCTTCATCCAGGTGTGCACCCAGCTGCAGGTGCTGACAGA  
GGCCTTCCGGGAGAAGGACACAGCTGTACAAGGCAACATCCGGCTCAGCTTCGAGGACTTCGTCA  
CCATGACAGCTTCTCGGATGCTATGACCCAACCATCTGTGGAGAGTGGAGTGCACCAGGGACCTT  
TCCTGGCTTCTTAGAGTGAGAGAAGTATGTGGACATCTCTTCTTTCTGTCCCTCTAGAAGAAC  
ATTCTCCCTTGCTTGATGCAACACTGTTCCAAAAGAGGGTGGAGAGTCTGCATCATAGCCACCA  
AATAGTGAGGACCGGGGCTGAGGCCACACAGATAGGGGCTGATGGAGGAGAGGATAGAAGTTGA  
ATGTCCTGATGGCCATGAGCAGTTGAGTGGCACAGCCTGGCACCAGGAGCAGGTCTTGTAATGG  
AGTTAGTGTCAGTCAGCTGAGCTCCACCCTGATGCCAGTGGTGAGTGTTTCATCGGCCTGTTACC  
GTTAGTACCTGTGTTCCCTCACCAGGCCATCCTGTCAAACGAGCCCATTTTCTCCAAAGTGAAT  
CTGACCAAGCATGAGAGAGATCTGTCTATGGGACCAGTGGCTTGGATTCTGCCACACCCATAAAT  
CCTTGTTGTGTTAACTTCTAGCTGCCTGGGGCTGGCCCTGCTCAGACAAATCTGCTCCCTGGGCAT  
CTTTGGCCAGGCTTCTGCCCCCTGCAGCTGGGACCCTCACTTGCTGCCATGCTCTGCTCGGCT  
TCAGTCTCCAGGAGACAGTGGTCACCTCTCCCTGCCAATACTTTTTTTAATTTGCATTTTTTTTC  
ATTTGGGGCCAAAAGTCCAGTGAAATTGTAAGCTTCAATAAAAGGATGAAACTCTGA

## **FIGURE 62**

MASYPYRQGCPGAAGQAPGAPPGSYYPGPPNSGGQYGSGLPPGGGYGGPAPGGPYGPPAGGGPYG  
HPNPGMFPSGTPGGPYGGAAPGGPYGQPPSSYGAQQPGLYGQGGAPPNVDPEAYSWFQSVDSDH  
SGYISMKELKQALVNCNWSSFNDETCLMMINMFDKTKSGRIDVYGFSALWKFIQQWKNLFQQYDR  
DRSGSISYTELQQALSQMGYNLSPQFTQLLVSRYCPRSANPAMQLDRFIQVCTQLQVLTEAFREK  
DTAVQGNIRLSFEDFVTMTASRML

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**N-glycosylation site.**

amino acids 147-150

**Casein kinase II phosphorylation sites.**

amino acids 135-138, 150-153, 202-205, 271-274

**N-myristoylation sites.**

amino acids 9-14, 15-20, 19-24, 33-38, 34-39, 39-44, 43-48, 61-66, 70-75, 78-83, 83-88, 87-92, 110-115

## FIGURE 63

CAGGATGCAGGGCCGCGTGGCAGGGAGCTGCGCTCCTCTGGGCCTGCTCCTGGTCTGTCTTCATC  
TCCCAGGCCTCTTTGCCCGGAGCATCGGTGTTGTGGAGGAGAAAGTTTCCCAAACTTCGGGACC  
AACTTGCCCTCAGCTCGGACAACCTTCCTCCACTGGCCCCCTCTAACTCTGAACATCCGCAGCCCCG  
TCTGGACCCTAGGTCTAATGACTTGGCAAGGGTTCCCTCTGAAGCTCAGCGTGCCTCCATCAGATG  
GCTTCCCACCTGCAGGAGGTTCTGCAGTGCAGAGGTGGCCTCCATCGTGGGGGGCTGCCTGCCATG  
GATTCCTGGCCCCCTGAGGATCCTTGGCAGATGATGGCTGCTGCGGCTGAGGACCGCCTGGGGGA  
AGCGCTGCCTGAAGAAGCTCTCTTACCTCTCCAGTGTGCGGCCCTCGCTCCGGGCAGTGGCCCTT  
TGCCTGGGGAGTCTTCTCCCGATGCCACAGGCCTCTCACCTGAGGCTTCACTCCTCCACCAGGAC  
TCGGAGTCCAGACGACTGCCCCGTTCTAATTCAGTGGGAGCCGGGGGAAAAATCCTTTCCCAACG  
CCCTCCCTGGTCTCTCATCCACAGGGTTCTGCCTGATCACCCCTGGGGTACCCTGAATCCCAGTG  
TGTCTGGGGAGGTGGAGGCCCTGGGACTGTTGGGGAACGAGGCCCATGCCACACCTGAGGGA  
ATCTGGGGTATCAATAATCAACCCCCAGGTACCAGCTGGGGAAATATTAATCGGTATCCAGGAGG  
CAGCTGGGGAAATATTAATCGGTATCCAGGAGGCAGCTGGGGGAATATTAATCGGTATCCAGGAG  
GCAGCTGGGGGAATATTCTATATACCCAGGTATCAATAACCCATTTCTCCTGGAGTTCTCCGC  
CCTCCTGGCTCTTCTTGGAACATCCCAGCTGGCTTCCCTAATCCTCCAAGCCCTAGGTTGCAGTG  
GGGCTAGAGCACGATAGAGGGAAACCCAACATTGGGAGTTAGAGTCCTGCTCCCGCCCCCTTGCTG  
TGTGGGCTCAATCCAGGCCCTGTTAACATGTTTCCAGCACTATCCCCACTTTTCAGTGCCTCCCC  
TGCTCATCTCCAATAAAATAAAAGCACTTATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAA

## **FIGURE 64**

MQGRVAGSCAPLGLLLVCLHLPGLFARSIGVVEEKVSQNFGTNLPQLGQPSSTGPSNSEHPQPAL  
DPRSNDLARVPLKLSVPPSDGFPPAGGSAVQRWPPSWGLPAMDSWPPEDPWQMAAAAEDRLGEA  
LPEELSYLSSAAAALAPGSGPLPGESSPDATGLSPEASLLHQDSESRRLPNSNLGAGGKILSQRP  
PWSLIHRVLPDHPWGTILNPSVSWGGGGPGTGWGTRMPHPHPEGIWGINNQPPGTSWGNINRYPGGS  
WGNINRYPGGSWGNINRYPGGSWGNIHLYPGINNPFPFGVLRPPGSSWNIPAGFPNPPSPRLQWG

Important features of the protein:

Signal peptide:

amino acids 1-26

Casein kinase II phosphorylation sites.

amino acids 56-59, 155-158

N-myristoylation sites.

amino acids 48-53, 220-225, 221-226, 224-229, 247-252, 258-263,  
259-264, 269-274, 270-275, 280-285, 281-286, 305-310

## **FIGURE 65**

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGGGTC  
TGGGCTGCCCCCTTGTCCTCCTCTTGACCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGA  
CTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAA  
TTGCTTGAAAAGCTCTGCCCTCCTCCATCTCCCTTCAGGGACCAGCGTCACCCTCCACCATGC  
AAGATCTCAACACCATGTTGTCTGCAACACATTGACAGCCATTGAAGCCTGTGTCCTTCTTGGCCC  
GGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCCTGTCTTTCAGCAGGCCCCACCCTC  
CTGAGTGGCAATAAATAAAATTCGGTATGCTG

## **FIGURE 66**

MSGGLPLVLLLTLLGSSHGTGPGMTLQLKLKESFLTNSSYESSFLELLEKLCLLLHLPSTSVTL  
HHARSQHHVVCNT

Important features:

Signal peptide:

amino acids 1-19

N-glycosylation site.

amino acids 37-41

N-myristoylation sites.

amino acids 15-21, 19-25, 60-66

## FIGURE 67

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCCGGGC  
CAGGTGCCCCGTCGCAGGTGCCCCCTGGCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGAAGCCCC  
TTCCTCGGCGCTGCCAACCCGCCACCCAGCCCATGGCGAACCCCGGGCTGGGGCTGCTTCTGGCG  
CTGGGCCTGCCGTTCTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACAGACCACTTCTGC  
AAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATGGCAACCTGCGTCCGG  
AAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTGCTCCTGGCTGTGGGGCTG  
GCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGGCACCTACCGGCCAGTAGCGA  
GGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGGACTCCAAGGAGACGGTGCAGGGCT  
GCCTGCCCATCTAGGTCCCCTCTCCTGCATCTGTCTCCCTTCATTGCTGTGTGACCTTGGGGAAA  
GGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAGTGCTTAATAGCAGGGAAGAAGGTACTTCAA  
AGACTCTGCCCCTGAGGTCAAGAGAGGATGGGGCTATTCACTTTTATATATTTATATAAAATTAG  
TAGTGAGATGTAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 68**

MANPGLGLLLALGLPFLRLARWGRAWGQIQTTSANENSTVLPSSSTSSSSDGNLRPEAITAIIVVFS  
LLAALLLAVGLALLVRKLRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

### **Important features:**

#### **Signal peptide:**

amino acids 1-19

#### **Transmembrane domain:**

amino acids 56-80

#### **N-glycosylation site.**

amino acids 36-40

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 86-90

#### **Tyrosine kinase phosphorylation site.**

amino acids 86-94

#### **N-myristoylation sites.**

amino acids 7-13, 26-32



## FIGURE 69

GCCAGGAATACTAGAGAGGAACAATGGGGTTATTGAGAGGTTTTGTTTTCTCTTAGTTCTGTGCCTGCTGCACCAG  
 TCAATACTTCTCTCATTAGCTGAATAATAATGGCTTGAAGATATTGTCATTGTTATAGATCCTAGTGTGCCAGAA  
 GATGAAAAATAATTGAACAAATAGAGGATATGGTGACTACAGCTTCTACGTACCTGTTTGAAGCCACAGAAAAAGA  
 TTTTTTTTTCAAAAATGTATCTATATTAATCTCTGAGAATTGGAAGGAAAACTCAGTACAAAAAGCCAAAACATGAA  
 AACCATAAACATGCTGATGTTATAGTTGCACCACCTACACTCCCAGGTAGAGATGAACCATACACCAAGCAGTTTACA  
 GAATGTGGAGAGAAAGGCGAATACATTCACTTCACCCCGACCTTCTACTTGGAAAAAACAAAATGAATATGGACCA  
 CCAGGCAAACTGTTTGTCCATGAGTGGGCTCACCTCCGGTGGGGAGTGTGATGAGTACAATGAAGATCAGCCTTTC  
 TACCGTGGCTAAGTCAAAAAAATCGAAGCAACAAGGTGTTCCGCAGGTATCTCTGGTAGAAATAGAGTTTATAAGTGT  
 CAAGGAGGCGAGTGTCTTAGTAGAGCATGCAGAATTGATTCTACAACAAACTGTATGGAAAAGATTGTCAATTCTTT  
 CCTGATAAAGTACAAACAGAAAAAGCATCCATAATGTTTATGCAAAGTATTGATTCTGTTGTTGAATTTGTAAACGAA  
 AAAACCCATAATCAAGAAGCTCCAAGCCTACAAAACATAAAGTGCAATTTTAGAAGTACATGGGAGGTGATTAGCAAT  
 TCTGAGGATTTTAAAAACACCATACCCATGGTGACACCACCTCCTCCACCTGTCTTCTCATTGCTGAAGATCAGTCAA  
 AGAATTGTGTGCTTAGTTCTTGATAAGTCTGGAAGCATGGGGGTAAGGACCGCTAAATCGAATGAATCAAGCAGCA  
 AAACATTTCTGCTGCAGACTGTTGAAAATGGATCCTGGGTGGGGATGGTTCACCTTTGATAGTACTGCCACTATTGTA  
 AATAAGCTAATCCAAATAAAAAGCAGTGATGAAAGAAACACACTCATGGCAGGATTACCTACATATCCTCTGGGAGGA  
 ACTTCCATCTGCTCTGGAATTAATATGCAATTCAGGTGATTGGAGAGCTACATCCCAACTCGATGGATCCGGAAGTA  
 CTGCTGCTGACTGATGGGAGGATAACACTGCAAGTCTTGTATTGATGAAGTGAACAAAGTGGGGCCATTGTTTATGTT  
 TTTATTGCTTTGGGAAGAGCTGCTGATGAAGCAGTAATAGAGATGAGCAAGATAACAGGAGGAAGTCATTTTATGTT  
 TCAGATGAAGCTCAGAACAATGGCCTCATTGATGCTTTTGGGGCTCTTACATCAGGAAATCTGATCTCTCCAGAG  
 TCCCTTCAGCTCGAAAGTAAGGGATTAACTGTAATAGTAATGCTGGATGAACGACACTGTCTAATGATAGTACA  
 GTGGGAAAGGACCGTCTTCTCATCATGGAACAGTCTGCCTCCAGTATTCTCTCTGGGATCCCAAGTGGGAACA  
 ATAATGGAAAATTTACAGTGGATGCAACTTCCAAAATGGCCTATCTCAGTATTCAGGAACGCAAGGTGGGCACT  
 TGGGCATACAATCTTCAAGCCAAAGCGAAGCCAGAAACATTAATCTTACAGTAACCTTCTCGAGCAGCAATCTTCT  
 GTGCCTCCAATCACAGTGAATGCTAAAATGAATAAGGACGTAACAGTTCCTCCAGCCCAATGATTGTTTACGCAGAA  
 ATTCTACAAGGATATGTACCTGTTCTTGGAGCCAATGTGACTGCTTTCATTGAATCACAGAATGGACATACAGAAGTT  
 TTGGAATTTTGGATAATGGTGACGGCGTGATTCTTCAAGAATGATGGAGTCTACTCCAGGTATTTTACAGCATAT  
 ACAGAAAATGGCAGATATAGCTTAAAGTTTGGGCTCATGGAGGAGCAACACTGCCAGGCTAAAATTACGGCCTCCA  
 CTGAATAGAGCCGCTACATACCAAGCTGGGTAGTGAACGGGGAAATTGAAGCAACCCGCAAGACCTGAAATTGAT  
 GAGGATACTCAGACCACCTTGGAGGATTTAGCCGGAACAGCATCGGAGGTGCATTTGTGGTATCACAAGTCCCAAGC  
 CTTCCTTGCCTGACCAATACCCACCAAGTCAATCACAGACCTTGATGCCACAGTTTATGAGGATAAGATTATCTT  
 ACATGGACAGCACCAGGAGATAATTTGATGTTGAAAAAGTTCAACGTTATATCATAAGAATAAGTGCAAGTATTCTT  
 GATCTAAGAGACAGTTTTGATGATGCTCTTCAAGTAAATACTACTGATCTGTACCAAAAGGAGGCCAACTCCAAGGAA  
 AGCTTTGCATTTAAACAGAAATATCTCAGAAGAAATGCAACCCACATATTTATGCCATTAAAAAGTATAGATAAA  
 AGCAATTTGACATCAAAAGTATCCAACATTGCACAAGTAACTTTGTTTATCCCTCAAGCAAATCCTGATGACATTGAT  
 CCTACACCTACTCCTACTCCTACTCCTACTCCTGATAAAAGTCATAATTCTGGAGTTAATATTCTACGCTGGTATTG  
 TCTGTGATTGGGTCTGTTGTAATTGTTAACTTTATTTAAGTACCACCATTTGAACCTTAAACGAAGAAAAAATCTTC  
 AAGTAGACCTAGAAGAGAGTTTAAAAAACAAAAAATGTAAGTAAAGGATATTTCTGAATCTTAAATTCATCCCAT  
 GTGTGATCATAACTCATAAAAATAATTTAAGATGTCGGAAGGAGTACTTTGATTAAATAAAACACTCATGGATA  
 TGTAAAACTGTCAAGATTAAATTTAATAGTTTCATTTATTTGTTATTTTATTTGTAAGAAATAGTGATGAACAAAG  
 ATCCTTTTTCATACTGATACCTGGTTGTATATTATTTGATGCAACAGTTTTCTGAAATGATATTTCAAATTCATCAA  
 GAAATAAAAATCATCTATCTGAGTAGTCAAAATACAAGTAAAGGAGAGCAAAATAACAACATTTGGAAAAA  
 AA

## **FIGURE 70**

MGLFRGFVFLLVLCLLHQSNTSFIKLNNGFEDIVIVIDPSVPEDEKIEQIEDMVTASTYLFE  
ATEKRFFFKNVSILIPENWKENPQYKRPKHENHKHADVIVAPPTLPGRDEPYTKQFTECGEKGEY  
IHFTPDLLLGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATRCISAGISGRN  
RVYKCGGSCSLRACRIDSTTKLYGKDCQFFPDQVQTEKASIMFMQSIDSVVEFCNEKTHNQEAP  
SLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPVFSLLKISQRIVCLVLDKSGSMGGKDRNLNR  
MNQAAKHFLQTVENGSWVGMVHFDSTATIVNKLIQIKSSDERNTLMAGLPTYPLGGTSICSGIK  
YAFQVIGELHSQLDGSEVLLLLTDGEDNTASSCIDEVKQSGAIVHFIALGRAADEAVIEMSKITGG  
SHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLTLNSNAWMNDTVIIDSTVGKDTFFL  
ITWNSLPSPISLWDPSGTIMENFTVDATSKMAYLSIPGTAKVGTWAYNLQAKANPETLTITVTSR  
AANSSVPPITVNAKNKDVNSFPSPMIVYAEILQGYVPVLGANVTAFIESQNGHTEVLELLDNGA  
GADSFKNQGVYSRYFTAYTENGRYSLKVRAGGANTARLKLRPPLNRAAYIPGWVVNGEIEANPP  
RPEIDEDTQTTLDEFSRTASGGAFVVSQVPSLPLPDQYPPSQITDLDATVHEDKIIILTWTPGDN  
FDVGKVQRYIIRISASILDLRDSFDDALQVNTTDLSPKEANSKESFAFKPENISEENATHIFIAI  
KSIDKSNLTSKVSNIAQVTLFIPQANPDDIDPTPTPTPTPTPKSHNSGVNISTLVLSVIGSVVI  
VNFILSTTI

### **Signal peptide:**

amino acids 1-21

### **Putative transmembrane domains:**

amino acids 284-300, 617-633

### **Leucine zipper pattern.**

amino acids 469-491, 476-498

### **N-glycosylation site.**

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,  
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

## FIGURE 71

CTCCTTAGGTGAAACCCTGGGAGTAGAGTACTGACAGCAAAGACCGGAAAGACCATACGTCCTCCGGGCGAGGGGTGA  
CAACAGGTGTCTATCTTTTGTCTCGTGTGGCTGCCTTCTCTATTTCAAGGAAAGACGCCAAGGTAATTTTGACCCA  
GAGGAGCAATGATGTAGCCACCTCCTAACCTTCCCTTCTTGAACCCCGAGTTATGCCAGGATTTACTAGAGAGTGTCA  
ACTCAACCAGCAAGCGGCTCCTTCGGCTTAACCTTGTGGTTGGAGGAGAGAACCTTTGTGGGGCTGCGTTCTCTTAGCA  
GTGCTCAGAAGTACTTGCCTCAGGGTGGACCAGAAGAAAGGAAAGGTCCCTCTTGTCTGTGGCTGCACATCAGGAA  
GGCTGTGATGGGAATGAAGGTGAAACTTGGAGATTTCACTTCAGTCATTGCTTCTGCCTGCAAGATCATCTTTAAA  
AGTAGAGAAGCTGCTCTGTGTGGTGGTTAACTCCAAGAGGCAGAACTCGTTCTAGAAGGAAATGGATGCAAGCAGCTC  
CGGGGGCCCCAAACGCATGCTTCTGTGGTCTAGCCCAGGGAAGCCCTTCCGTGGGGCCCCGGCTTTGAGGGATGCC  
ACCGGTTCTGGACGCATGGCTGATTCCTGAATGATGATGTTTCGCCGGGGGCTGCTTGCCTGGATTTCCCGGGTGGTG  
GTTTGTGTGGTCTCTCTGTCTGTCTATCTCTGTCTGTACATGTTGGCTGCACCCCAAAGGTGACGAGGAGCAG  
CTGGCACTGCCACGGGCCAACAGCCCCACGGGAAGGAGGGGTACCAGGCCGCTCCTTCAGGAGTGGGAGGAGCAGCAC  
CGCAACTACGTGAGCAGCCTGAAGCGGCAGATCGCACAGCTCAAGGAGGAGCTGCAGGAGAGGAGTGAGCAGCTCAGG  
AATGGGCAGTACCAAGCCAGCGATGCTGCTGGCCTGGGTCTGGACAGGAGCCCCCAGAGAAAACCCAGGCCGACCTC  
CTGGCCTTCTGTCACTCGCAGGTGGACAAGGCAGAGGTGAATGCTGGCGTCAAGCTGGCCACAGAGTATGCAGCAGTG  
CCTTTCGATAGCTTTACTCTACAGAAGGTGTACCAGCTGGAGACTGGCCTTACCGGCCACCCGAGGAGAAGCCTGTG  
AGGAAGGACAAGCGGGATGAGTTGGTGGAAAGCCATTGAATCAGCCTTGGAGACCTGAACAATCTGCAGAGAACAGC  
CCCCATCACCGTCTTACACGGCTCTGATTTCTAGAAAGGGATCTACCGAACAGAAAGGGACAAGGGACATTGTAT  
GAGCTCACCTTCAAAGGGGACCAACAAACAGGAATTCAAACGGCTCATCTTATTTGACCATTCAGCCCCATCATGAAA  
GTGAAAAATGAAAGCTCAACATGGCCAAACAGCCTTATCAATGTTATCGTGCCTCTAGCAAAAAGGTTGGACAGTTC  
CGGCAGTTTCATGAGAATTTCAAGGAGATGTGCATTGAGCAGGATGGGAGAGTCCATCTCACTGTTGTTACTTTGGG  
AAGAGAAGAAATAAATGAAGTCAAAGGAATACTTGAAACACTTCAAAGCTGCCAATTCAGGAACCTTTACCTTCATC  
CAGCTGAATGGAGAATTTCTCGGGGAAAGGACTTGATGTTGGAGCCCGCTTCTGGAAGGGAAGCAACCTCCTTCTC  
TTTTTCTGTGATGGACATCTACTTCACATCTGAATTCCTCAATACGTGTAGGCTGAATACACAGCCAGGGAAGAG  
GTATTTTATCCAGTCTTTTCAGTCAGTACAAATCCTGGCATAATATACGGCCACCATGATGCAGTCCCTCCCTTGGAA  
CAGCAGCTGGTCATAAAGAGGAACTGGATTTTGGAGAGACTTTGGATTTGGGATGACGTGTGATGTCAGTATCGGTGAGC  
TTCATCAATATAGGTGGGTTTGTCTGGACATCAAAGGCTGGGGCGGAGAGGATGTGCACCTTTATCGCAAGTATCTC  
CACAGCAACCTCATAGTGTACCGACGCTGTGGCAGGACTCTTCCACCTCTGGCATGAGAAGCGCTGCATGGACGAG  
CTGACCCCCGAGCAGTACAAGATGTGCATGCAAGTCCAAGGCCATGAACGAGGCATCCACGGCCAGCTGGGCATGCTG  
GTGTTCAAGCAGAGATAGAGGCTCACCTTCGCAACAGAAACAGAGACAGTAGCAAAAAACATGAAGTCCCAGA  
GAAGGATTGTGGGAGACACTTTTCTTCCCTTTTGAATTAAGTGGCTGCAACAGAGAAAAGACTTCCATAAA  
GGACGACAAAAGAAATGGACTGATGGGTGAGAGATGAGAAAGCCTCCGATTTCTCTCTGTTGGGCTTTTACAACAGA  
AATCAAAATCTCCGCTTTGCCCTGCAAAAGTAACCCAGTTGCACCTGTGAAGTGTCTGACAAAGGCAGAAATGCTTGTG  
AGATTATAAGCCTAATGGTGTGGAGGTTTGTGAGTGTGTTACAATACACTGAGACCTGTTGTTTGTGTGCTCATGGA  
AATATTCATGATTTAAGAGCAGTTTGTAAAAAATTCATTAGCATGAAAGGCAAGCATATTTCTCCTCATATGAATGA  
GCCTATCAGCAGGGCTCTAGTTTCTAGGAATGCTAAAAATTCAGAAGGCAGGAGAGGAGATAGGCTTATTATGATACT  
AGTGAGTACATTAAAGTAAATAAATGGACCAGAAAAGAAAAGAACCATAAATATCGTGTCTATTTTCCCCAAGAT  
TAACCAAAAATAATCTGCTTATCTTTTGGTTGTCTTTAACTGTCTCCGTTTTTTCTTTTATTTAAAAATGCAT  
TTTTTTCCCTTGTGAGTTATAGTCTGCTTATTTAATTACCACTTTGCAAGCCTTACAAGAGAGCACAAAGTTGGCCTAC  
ATTTTATATTTTTTAAAGATACTTTGAGATGCAATATGAGAACTTCAGTTCAAAGCATCAAATGATGCCATAT  
CCAAGGACATGCCAAATGCTGATTCGTGAGGCACTGAATGTCAGGCATTGAGACATAGGGAAGGAATGGTTGTACT  
AATACAGACGTACAGATACTTTCTGGAAGATATTTTGAAGAGGAGCAACTGAACACTGGAGGAAAAGAAAATGAC  
ACTTTCTGCTTTACAGAAAAGGAACTCATTGAGACTGGTGATATCGTGATGTACCTAAAAGTCAGAAACCAATTTT  
CTCCTCAGAAGTAGGGACCGCTTCTTACCTGTTTAAATAAACCAAGTATACCGTGTGAACCAACCAATCTCTTTT  
AAAACAGGGTGTCTCCTCTGGCTTCTGGCTTCCATAAGAAAGAAATGGAGAAAATATATATATATATATATATATTGT  
GAAAGATCAATCCATCTGCCAGAATCTAGTGGGATGGAAGTTTTTGTACATGTTATCCACCCAGGCCAGGTGGAAG  
TAACTGAATTTATTTTAAATTAAGCAGTTCTACTCAATCACCAGATGCTTCTGAAAATGCAATTTTATTACCATTT  
CAAATATTTTTTAAAAATAAATACAGTTAATACATAGAGTGGTTTCTTCATTGATGTGAAAATTTATTAGCCAGCAG  
ATGCATGAGCTAATTTATCTCTTTGAGTCTTGTCTTCTGTTTGTCTCAGAGTAACTCATTTGTTTAAAGCTTCAAGAAC  
ATTCAAGCTGTTGGTGTGTTAAAAATGCATTGTATTGATTGTACTGGTAGTTTATGAAATTTAATTAACACAGG  
CCATGAATGGAAGGTGGTATTGCACAGCTAATAAATATGATTTGTGGATATGAA

## **FIGURE 72**

MMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQLALPRANSPGKEGYQAVLQEW  
EQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFLHSQVDK  
AEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVKDKRDELVEAIESALETLNPA  
ENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSPIMKVKNELNMAN  
TLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVKGILENTSKAANFRNF  
TFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNLCRLNTQPGKKVFYPVLF  
SQQY  
NPGIIYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFDDIKGWGGEDVHLYR  
KYLHNSNLIVRTPVRGLFHLWHEKRCMDLTPEQYKMCMSKAMNEASHGQLGMLVFRHEIEAHL  
RKQKQKTSSKKT

### **Important features:**

#### **Signal peptide:**

amino acids 1-27

#### **N-glycosylation sites.**

amino acids 315-319, 324-328

#### **N-myristoylation sites.**

amino acids 96-102, 136-142, 212-218, 311-317, 339-345, 393-399

#### **Amidation site.**

amino acids 377-381

Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

## **FIGURE 74**

MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPDLPALQ  
PHGYDQPGTEPLDLHNNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKSGPGGSEHQINSEAT  
FAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPP  
FNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTEEEPSKLLV  
QNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYFIARKIRKKRLENRKS  
VVFTSAQATTEA

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-15

#### **Transmembrane domain:**

amino acids 291-310

#### **N-glycosylation site.**

amino acids 213-216

#### **Eukaryotic-type carbonic anhydrases proteins**

amino acids 197-245, 104-140, 22-69

## FIGURE 75

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCCCTTGGGGACGGGCAGTTCCTGTGTC  
TCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGAATGTCCTACA  
ATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATTTTCATCACAA  
ATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTCTGTGTCTGACAGCTCC  
AGAGAAGTGGAAGAGAAATCCAGAAGACCTTCTGTTTCCATGCAACAAATATACTCCAATCTGA  
AGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCCCAGTGTGTGACCAACCAC  
ACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGTACACGTGGAGTCCTTCGTCCC  
AGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTGCCAGGACTTTGAAAGATCAATCAT  
CAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTTTGCCATATCTATTACCGTGTTCCTTTTT  
TCTGTGATGGGCTIATTCATCTACCGATATATCCACGTTGGCAAAGAGAAACACCCAGCAAATTT  
GATTTTGATTTATGAAATGAATTTGACAAAAGATTCTTTGTGCCTGCTGAAAAATCGTGATTA  
ACTTTATCACCTCAATATCTCGGATGATTCTAAAATTTCTCATCAGGATATGAGTTTACTGGGA  
AAAAGCAGTGATGTATCCAGCCTTAATGATCCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGA  
GGAAGAGGAGGTGAAACATTTAGGGTATGCTTCGCATTTGATGGAAATTTTTTGTGACTCTGAAG  
AAAACACGGAAGGTACTTCTCTACCCAGCAAGAGTCCCTCAGCAGAACAATACCCCCGGATAAA  
ACAGTCATTGAATATGAATATGATGTCAGAACCACTGACATTTGTGCGGGGCCCTGAAGAGCAGGA  
GCTCAGTTTGCAGGAGGAGGTGCCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTTGCCAG  
TCTTGGGCCCCGAAACGTTACAGTACTCATAACCCCTCAGCTCCAAGACTTAGACCCCTGGCG  
CAGGAGCACACAGACTCGGAGGAGGGCCGGAGGAAGAGCCATCGACGACCCTGGTCGACTGGGA  
TCCCCAACTGGCAGGCTGTGTATTCTTCGCTGTCCAGCTTCGACCAGGATTCAGAGGGCTGCG  
AGCCTTCTGAGGGGATGGGCTCGGAGAGGAGGTCTTCTATCTAGACTCTATGAGGAGCCGGCT  
CCAGACAGGCCACCAGGAGAAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGGTTATA  
TGTGCAGATGGAAAACTGATGCCAACACTTCCTTTTGCCTTTTGTTCCTGTGCAAACAAGTGAG  
TCACCCCTTTGATCCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTCCAGTTTGTGAGTGT  
CTGTGAGAATTACTTATTTCTTTCTCTATTCTCATAGCACGTGTGTGATTGGTTCATGCATGTA  
GGTCTCTTAACAATGATGGTGGCCCTCTGGAGTCCAGGGGCTGGCCGGTTGTTCTATGCAGAGAA  
AGCAGTCAATAAATGTTTGCCAGACTGGGTGCAGAATTTATTAGGTGGGTGT

## **FIGURE 76**

MSYNGLHQRVFKELKLLTLCSISSQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIY  
SNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQCARTLK  
DQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILYGNFDRFFVPAEK  
IVINFITLNISSDKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKHLGYASHLMEIFC  
DSEENTEGTSLTQQESLSRTIPDPKTVIEYDYDVRTTDICAGPEEQELSLQEEVSTQGTLLSQA  
ALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEPPSTTLVDWDPQTGRLCIPSLSSFDQDS  
EGCEPSEGDGLGEEGLLSRLYEPPAPDRPPGENETYLMQFMEEWGLYVQMEN

**Important features:**

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 140-163

**N-glycosylation sites.**

amino acids 71-74, 80-83, 89-92, 204-207, 423-426



## FIGURE 77

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCACTTGCTGCCCTCTGACAC  
CTGGGAAGATGCCCCGCGCGTGGACCTTCACCCCTTCTCTGTGGTTTGCTGGCAGCCACCTTGATC  
CAAGCCACCCTCAGTCCCACTGCAGTTCTCATCCTCGGCCCAAAGTCATCAAAGAAAAGCTGAC  
ACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGCTCAGTGCCATGC  
GGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCTGGTGAACACCGTCCTGAAGCACATC  
ATCTGGCTGAAGGTCATCACAGCTAACATCCTCCAGCTGCAGGTGAAGCCCTCGGCCAATGACCA  
GGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCAACACGCCCTGGTCAAGACCA  
TCGTGGAGTTCACATGACGACTGAGGCCCAAGCCACCATCCGCATGGACACCAGTGCAAGTGGC  
CCCACCCGCTGGTCCCTCAGTGACTGTGCCACCAGCCATGGGAGCCTGCGCATCCAAGTGTGTA  
TAAGCTCTCCTTCCTGGTGAACGCCTTAGCTAAGCAGGTGATGAACCTCCTAGTGCCATCCCTGC  
CCAATCTAGTGAAAAACCAGCTGTGTCCCGTGATCGAGGCTTCCTTCAATGGCATGTATGCAGAC  
CTCCTGCAGCTGGTGAAGGTGCCATTTCCTCAGCATTGACCGTCTGGAGTTTGACCTTCTGTA  
TCCTGCCATCAAGGGTGACACCATTAGCTCTACCTGGGGGCCAAGTTGTTGGACTCACAGGGAA  
AGGTGACCAAGTGGTTCAATAACTCTGCAGCTTCCTTGACAATGCCACCCTGGACAACATCCCG  
TTCAGCCTCATCGTGAGTCAGGACGTGGTGAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGA  
ATTCATGGTCTGTTGGACTCTGTGCTTCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGC  
TGATCAATGAAAAGGCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGAC  
ACTCCCGAGTTTTTTATAGACCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGCTGGAAGTGTT  
TCCCTCCAGTGAAGCCCTCCGCCCTTTGTTACCCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGT  
TTTACACCAAAGGTGACCAACTTATACTCAACTTGAATAACATCAGCTCTGATCGGATCCAGCTG  
ATGAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCCA  
CTCCATCCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTCATTGGTGAAGG  
CCTTGGGATTCGAGGCAGCTGAGTCCCTCACTGACCAAGGATGCCCTTGTGCTTACTCCAGCCTCC  
TTGTGGAAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAGGGAAGGCTGG  
GTCCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAATCAATAAACACTTG  
CCTGTGAAAAA

## **FIGURE 78**

MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILQQPLLSAMREK  
PAGGIPVLGSLVNTVLKHIIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPLVKTIVE  
FHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMNLLVPSLPNL  
VKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDTIQLYLGAKLLDSQGKVT  
KWFNNSAASLTMPITLDNIPFSLIVSQDVVKAAVAVALSPPEEFMVLLDSVLPESAHLKSSIGLIN  
EKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSEALRPLFTLGIEASSEAQFYT  
KGDQLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIIHSILLPNQNGKLRSGVPVSLVKALG  
FEAAESSLTkdalvltPASLWKpSSPVsq

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 48-51, 264-267, 401-404

**Glycosaminoglycan attachment site.**

amino acids 412-415

**LBP / BPI / CETP family proteins.**

amino acids 407-457

## FIGURE 79

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAGAGC  
TTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCCATGGCCTCT  
CTTGGCCTCCAACCTTGTGGGTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACTGGTTGCCAT  
GCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTGGTGCCAGCATTGTGACAGCAGTTGGCTTCT  
CCAAGGGCCTCTGGATGGAATGTGCCACACAGCACAGGCATCACCCAGTGTGACATCTATAGC  
ACCCCTTCTGGGCCTGCCCCGCTGACATCCAGGCTGCCAGGCCATGATGGTGACATCCAGTGCAAT  
CTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCACAGTCTTCTGCCAGGAATCCC  
GAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTCATCCTTGAGGGCCTCCTGGGATTC  
ATTCTGTTCCTGGAATCTTCATGGGATCCTACGGGACTTCTACTCACCCTGGTGCCTGACAG  
CATGAAATTTGAGATTGGAGAGGCTCTTTACTTGGGCATTATTTCTTCCCTGTTCTCCCTGATAG  
CTGGAATCATCTCTGCTTTTCTGCTCATCCCAGAGAAATCGTCCAACCTACTACGATGCCTAC  
CAAGCCCAACCTCTTGCCACAAGGAGCTCTCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGA  
GTTCAATTCTACAGCCTGACAGGGTATGTGTGTAAGAACCAGGGGCCAGAGCTGGGGGGTGGCTG  
GGTCTGTGAAAAACAGTGGACAGCACCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGT  
GTCAGAAGGTGCTGCTGAGGATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGG  
GCTAGTGTAACAGCATGCAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCC  
TCACCTTGCTGCTCCCCTGCCCTAAGTCCCCAACCTCAACTTGAAACCCCATTCCTTAAGCCA  
GGACTCAGAGGATCCCTTTGCCCTCTGGTTTACCTGGGA<sup>CT</sup>CCATCCCCAAACCCACTAATCACA  
TCCCACTGACTGACCCTCTGTGATCAAAGACCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATT  
GCTGGGGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTC  
CCTCCAAAGAACTGATTGGCCCTGGAACCTCCATCCCACTCTTGTTATGACTCCACAGTGTCCA  
GACTAATTTGTGCATGAACTGAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAGGATG  
CAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

## **FIGURE 8o**

MASLGLQLVGYYLGLLGLLGLTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGITQCD  
IYSTLLGLPADIQAAQAMMVTSSAISSLACIISVVGMRCTVFCQESRAKDRVAVAGGVFFILGGL  
LGFIPVAVNNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCSSQRNRSNYY  
DAYQAQPLATRSSPRPGQPPKVKSEFNYSYSLTGYV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-24

**Transmembrane domains:**

amino acids 82-102, 117-140, 163-182

**N-glycosylation site.**

amino acids 190-193

**PMP-22 / EMP / MP20 family proteins.**

amino acids 46-59

## FIGURE 81

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCTTTC  
CCCCGCTTCTCTTTCCACCTTTCTCTTCTTCCACCTTAGACCTCCCTTCCTGCCCTCCTTTTCCT  
GCCCACGCTGCTTCTTGGCCCTTCTCCGACCCGCTCTAGCAGCAGACCTCCTGGGGTCTGTGG  
GTTGATCTGTGGCCCCGTGCTTCCGTGTCTTTTCGTCTCCCTTCCTCCGACTCCGCTCCCGG  
ACCAGCGCCTGACCCTGGGGAAAGGATGGTTCCCGAGGTGAGGGTCTCTCCTCCTTGCTGGGA  
CTCGCGTGTCTGGTTCCCCCTGGACTCCCACGCTCGAGCCCGCCAGACATGTTCTGCCTTTT  
CCATGGGAAGAGATACTCCCCGGCGAGAGCTGGCACCCCTACTTGGAGCCACAAGGCCTGATGT  
ACTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGTTGTTACCGCCTCCACTGTCCGCT  
GTCCACTGCCCCCAGCCTGTGACGGAGCCACAGCAATGCTGTCCCAAGTGTGTGGAACCTCACAC  
TCCCTCTGGACTCCGGGGCCCCACCAAAGTCTGCCAGCACAACGGGACCATGTACCAACACGGAG  
AGATCTTCAGTGCCCATGAGCTGTTCCCTCCCGCTGCCCAACCAGTGTGTCTCTGCAGTGC  
ACAGAGGGCCAGATCTACTGCGGCCTCACAACCTGCCCCGAACCAGGCTGCCCAGACCCCTCCC  
ACTGCCAGACTCCTGCTGCCAAGCCTGCAAAGATGAGGCAAGTGAAGCAATCGGATGAAGAGGACA  
GTGTGCAGTCGCTCCATGGGGTGAGACATCCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAG  
AGAGGCCCCGGGCACCCCAAGCCCCACTGGCCTCAGCGCCCCTCTGAGCTTCATCCCTCGCCACTT  
CAGACCCAAGGGAGCAGGCAGCACAACCTGTCAAGATCGTCTGAAGGAGAAACATAAGAAAGCCT  
GTGTGCATGGCGGGAAGACGTACTCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGC  
CCCTTGCCCTGCATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCC  
CACCGAGTACCCCTGCCGTACCCCGAGAAAGTGGCTGGGAAGTGTGCAAGATTTGCCCAGAGG  
ACAAAGCAGACCCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCCGGGTC  
CTCGTCCACACATCGGTATCCCCAAGCCCAGACAACCTGCGTCGCTTTGCCCTGGAACACGAGGC  
CTCGGACTTGGTGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAACTGAGGCTCAGAGAG  
GTGAAGTACCTGGCCCAAGGCCACACAGCCAGAATCTTCCACTTGAATCAGATCAAGAAAGTCAG  
GAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCACGAAGGTCACT  
GGAACGTCTTCTAGCCCAGACCCTGGAGCTGAAGGTCACGGCCAGTCCAGACAAAGTGACCAAG  
ACATAACAAAGACCTAACAGTTGCAGATATGAGCTGTATAATTGTTGTTATTATATATTAATAAA  
TAAGAAGTTGCATTACCCTCAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 82**

MVPEVRVLSSLLGLALLWFPLDSHARARPDMFCLFHGKRYSPGESWHPYLEPQGLMYCLRTCSE  
GAHVSCYRLHCPPVHCPQPVTEPQQCCPKCVPHTPSGLRAPPKSCQHNGTMYQHGEIFSAHELF  
PSRLPNQCVLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEEDSVQSLHGVR  
HPQDPCSSDAGRKRGPPTAPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKHKACVHGGKTYS  
HGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPTTEYPCRHPEKVAGKCKICPEDKADPGHSE  
ISSTRCPKAPGRVLVHTSVSPDNLRRFALEHEASDLVEIYLWKLVKDEETEAQRGEVPGPRPH  
SQNLPLDSDQESQEARLPERGTALPTARWPFRSLERLPSPDPAEGHGQSRQSDQDITKT

**Signal peptide:**

amino acids 1-25

## FIGURE 83

GACAGCTGTGCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTGCCCTCCGCTCACGCAGAGCCTCTCC  
GTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTTCTCTCTAATCCATCCGTCACCTCTCCTGTCA  
TCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCCATGGCTCTCATGCTCAGTTTGGTTCTGAGTC  
TCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTTGGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGGAG  
GACGCAGCATTCTCCTGTTTCTGTCTCCTAAGACCAATGCAGAGGCCATGGAAGTGCGGTTCTTCAGGGG  
CCAGTTCTCTAGCGTGGTCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATC  
AAGGCAGGACAAAACCTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGGAACATTACT  
GTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCAGTCTTACTACCAGAAGGCCATCTGGGAGCT  
ACAGGTGTGAGCACTGGGCTCAGTTCTCTCATTTCCATCACGGGATATGTTGATAGAGACATCCAGCTAC  
TCTGTCTGCTCGGGCTGGTTCCCCCGGCCACAGCGAAGTGAAAGGTCCACAAGGACAGGATTTGTCC  
ACAGACTCCAGGACAAACAGAGACATGCATGGCCTGTTTGATGTGGAGATCTCTCTGACCGTCCAAGAGAA  
CGCCGGGAGCATATCCTGTTCCATGCGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAG  
GAGATACCTTTTTTCGAGCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTA  
TTTTTTGGCATTGTGGACTGAAGATTTTCTTCTCCAAATTCAGTGGAAAATCCAGGCGGAACCTGGACTG  
GAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCCGAAACACGCAGTGGAGGTGACTCTGGATCCAG  
AGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAACCTGTAACCCATAGAAAAGCTCCCCAGGAGGTG  
CCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCTTCTCAGAGTTTCCAAGCAGGGAACATTA  
CTGGGAGGTGGACGGAGGACACAATAAAAGGTGGCGTGGGAGTGTGCCGGGATGATGTGGACAGGAGGA  
AGGAGTACGTGACTTTGTCTCCCGATCATGGGTACTGGGTCTCAGACTGAATGGAGAACATTTGTATTTC  
ACATTAAATCCCCGTTTTATCAGCGTCTTCCCCAGGACCCACCTACAAAAATAGGGGTCTTCTGGACTA  
TGAGTGTGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCGTGACATGTCGGTTTG  
AAGGCTTATTGAGGCCCTACATTGAGTATCCGTCCTATAATGAGCAAAATGGAACCTCCCATAGTCATCTGC  
CCAGTCACCCAGGAATCAGAGAAAGAGGCCTCTTGGCAAAGGGCCTCTGCAATCCCAGAGACAAGCAACAG  
TGAGTCCTCCTCACAGGCAACCACGCCCTTCTCCCCAGGGGTGAAATGTAGGATGAAATCACATCCCACAT  
TCTTCTTTAGGGATATTAAGGTCTCTCTCCAGATCCAAAGTCCCGCAGCAGCCGGCCAAAGGTGGCTTCCA  
GATGAAGGGGGACTGGCCTGTCCACATGGGAGTCAGGTGTATGGCTGCCCTGAGCTGGGAGGGAAGAAGG  
CTGACATTACATTTAGTTTGTCTCTCACTCCATCTGGCTAAGTGTCTTGAAATACCACCTCTCAGGTGAAG  
AACCGTCAGGAATCCCATCTCACAGGCTGTGGTGTAGATTAAAGTAGACAAGGAATGTGAATAATGCTTAG  
ATCTTATTGATGACAGAGTGTATCCTAATGGTTTGTTCATTATATTACACTTTCAGTAAAAAAA

## **FIGURE 84**

MALMLSLVLSLLKLGSGQWQVFGPDKPVQALVGEDAAFSCFLSPKTNAEAMEVRFFRGQFSSVVH  
LYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISQSYQKAIWELQ  
VSALGSVPLISITGYVDRDIQLLCQSSGWFPPTAKWKGPQGDLSTDSRTNRDMHGLFDVEISL  
TVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLFFGIVGLKIFFSK  
FQWKIQAELDWRRKHGQAEIRDARKHAVEVTLPETAHPKLCVSDLKTVTHRKAQEVPHSEKRF  
TRKSVVASQSFOAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTLSPDHGYWVLRNLNGEHLFT  
LNPRFISVFPRTPTTKIGVFLDYECGTISFFNINDQSLIYTLTCRFEGLLRPYIEYPSYNEQNGT  
PIVICPVTQESEKEASWQRASAIPESTNSSESSQATTPFLPRGEM

### **Signal peptide:**

amino acids 1-17

### **Transmembrane domain:**

amino acids 239-255



## FIGURE 85

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCAGACATGCTGCTGCTGCTGCTGCCCCT  
GCTCTGGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAACTGCTGACGATGCAGAGTTCCGTGA  
CGGTGCAGGAAGGCCTGTGTGTCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCATGGCTGGATT  
TACCCTGGCCCAGTAGTTTCATGGCTACTGGTTCCGGGAAGGGGCCAATACAGACCAGGATGCTCC  
AGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACCGATTCCACCTCCTTG  
GGGACCCACATACCAAGAATTGCACCCTGAGCATCAGAGATGCCAGAAGAAGTATGCGGGGAGA  
TACTTCTTTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAAACATCACCGGCTCTCTGTGAA  
TGTGACAGCCTTGACCCACAGGCCCAACATCCTCATCCCAGGCACCCCTGGAGTCCGGCTGCCCCC  
AGAATCTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAGGGGACACCCCTATGATCTCCTGGATA  
GGGACCTCCGTGTCCCCCTGGACCCCTCCACCACCCGCTCCTCGGTGCTCACCCCTCATCCCACA  
GCCCCAGGACCATGGCACCAGCCTCACCTGTCAGGTGACCTTCCCTGGGGCCAGCGTGACCACGA  
ACAAGACCGTCCATCTCAACGTGTCTACCCGCCTCAGAACTTGACCATGACTGTCTTCCAAGGA  
GACGGCACAGTATCCACAGTCTTGGGAAATGGCTCATCTCTGTCACTCCAGAGGGCCAGTCTCT  
GCGCCTGGTCTGTGCAGTTGATGCAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGA  
GAGGCCTGACCCTGTGCCCTCACAGCCCTCAAACCCGGGGTGCTGGAGCTGCCTTGGGTGCAC  
CTGAGGGATGCAGCTGAATTCACCTGCAGAGCTCAGAACCTCTCGGCTCTCAGCAGGTCTACCT  
GAACGTCTCCCTGCAGAGCAAAGCCACATCAGGAGTGA CTGAGGGGTGGTTCGGGGAGCTGGAG  
CCACAGCCCTGGTCTTCCTGTCTCTGCGTCATCTTCGTTGTAGTGAGGTCTGCAGGAAGAAA  
TCGGCAAGGCCAGCAGCGGGCGTGGGAGATACGGGCATAGAGGATGCAAACGCTGTGAGGGGTTT  
AGCCTCTCAGGGGCCCCCTGACTGAACCTTGGGCAGAAGACAGTCCCCCAGACCAGCCTCCCCCAG  
CTTCTGCCCGCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGTG  
AAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCCACAG  
ATGAGAAACTGCAGAGACTCACCTGATTGAGGGATCAGAGCCCTCCAGGCAAGGGAGAAGTCA  
GAGGCTGATTCTTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACTATGAATTATG  
TGCAGAGTGAAAAGCACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAATCCACACTGTGCCC  
TCCCTTTTATTTTTTAACTAAAAGACAGACAAATTCCTA

## **FIGURE 86**

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSYP SHGWIYPGPVVHGYWFREG  
ANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKGSIKWNY  
KHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCSPWACEQGTPPMISWIGTSVSPLDPSTTRS  
SVLTLIPQPQDHGTS LTCQVT FPGASVTTNKT VHLNVSYPQNLMTVFQGDGTVSTVLGNGSSL  
SLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWVHLRDAAEFTCRAQNP  
LGSQQVYLNVS LQSKATSGVTQG VVGAGATALVFLSFCVIFVVVRSCRKKSARPAAGVGD TGIE  
DANAVRGSASQGPLEPWAEDSPPDQPPASARSSVGE GELQYASLSFQMVKPWDSRGQEATDTE  
YSEIKIHR

### **Signal peptide:**

amino acids 1-15

### **Transmembrane domain:**

amino acids 351-370

## FIGURE 87

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTGTAC  
CCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGCTGTTTC  
TCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAATGGACCTGT  
TCTTCGTCTCCATCTCTGCCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCCTAGTGCAATTTGA  
TGGCCTGTATTTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTTCTGTGACATGACCTCTG  
GGGGTGGCGGCTGGACCCTGGTGGCCAGCGTGCATGAGAATGACATGCGTGGGAAGTGCACGGTG  
GGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCCAGAGGGGGACGGCAACTGGGC  
CAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCGATGACTACAAGAACCCTGGCTACT  
ACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTGCCCAATAAGTCCCCCATGCAGCACTGG  
AGAAACAGCTCCCTGCTGAGGTACCGCACGGACACTGGCTTCCTCCAGACACTGGGACATAATCT  
GTTTGGCATCTACCAGAAATATCCAGTGAAATATGGAGAAGGAAAGTGTGGACTGACAACGGCC  
CGGTGATCCCTGTGGTCTATGATTTTGGCGACGCCCAGAAAACAGCATCTTATTACTCACCTTAT  
GGCCAGCGGGAATTCAGTGCAGGATTTGTTTCAGTTCAGGGTATTTAATAACGAGAGAGCAGCCAA  
CGCCTTGTGTGCTGGAATGAGGGTCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAG  
GATACTTTCCAGAGGCCAGTCCCCAGCAGTGTGGAGATTTTCTGGTTTTGATTGGAGTGGATAT  
GGAACTCATGTTGGTTACAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCG  
TTGAGAGTTTTGTGGGAGGGAACCCAGACCTCTCCTCCCAACCATGAGATCCCAAGGATGGAGAA  
CAACTTACCCAGTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAAATCATATTGACTCAAGA  
AAAAAA

## **FIGURE 88**

MNQLSFLLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTENGVI  
YQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDWSSQQGSKADYPEGDGNWANYNTFGSAEAAT  
SDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGIYQKYPVKYG  
EGKCWTDNGPVI PVVYDFGDAQKTASYISPYGQREFTAGFVQFRVFNNERAANALCAGMRVTGCN  
TEHHCIGGGGYFPEASPQQCGDFSGFDWSGYGTHVGYSSSREITEAAVLLFYR

**Important features:**

**Signal peptide:**

amino acids 1-16

**N-glycosylation site.**

amino acids 163-167

**Glycosaminoglycan attachment sites.**

amino acids 74-78, 289-293

**N-myristoylation sites.**

amino acids 76-82, 115-121, 124-130, 253-259, 292-298

## FIGURE 89

CTAGATTGTGGCTTGGGGGAGACTTCAGGAGTCGCTGTCTCTGAACCTCCAGCCTCAGAGAC  
CGCCGCCCTTGTCCCCGAGGGCCATGGGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTCCTGACG  
CTCCTGGCGCATCTGGTGGTCGTACACCTTATTCTGGTCCCGGGACAGCAACATACAGGCCTG  
CCTGCCCTCTACGTTACCCCCGAGGAGTATGACAAGCAGGACATTTCAGCTGGTGGCCGCGCTCT  
CTGTACCCCTGGGCCTCTTTCAGTGGAGCTGGCCGGTTTCCTCTCAGGAGTCTCCATGTTCAAC  
AGCACCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGTGGCCCTGTCCTTCTTCAT  
ATTGAGCGTTGGGAGTGCACCTACGTATTGGTACATTTTGTCTTCTGCAGTGCCCTTCCAGCTG  
TCACTGAAATGGCTTTATTCGTACCGTCTTTGGGCTGAAAAGAAACCCCTTCGATTACCTTCA  
TGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGGCCGCTTCGTATTCTGGAAGAAGGAAG  
GCATAGGCTTCGGTTTTCCCTCGGAACTGCTTCTGCTGGAGGATATGTGTTGGAATAATTACG  
TCTTGAGTCTGGGATTATCCGCATTGTATTTAGTGCTTTGTAATAAAATATGTTTGTAGTAACA  
TTAAGACTTATATACAGTTTAGGGGACAATTAAAAAAAAAAAA

## **FIGURE 90**

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLGLFA  
VELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCALPAVTEMALFV  
TVFGLKKKPF

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

123456789101112131415161718192021222324252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899100

## FIGURE 91

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAGATGCAACTGAC  
TCGCTGCTGCTTCGTGTCTCTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGGATGATG  
GTCCTCCCGGCTCAGAGGACCCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCCCGGGTGCCT  
CGGAAGCGGGGCCACATCTCACCTAAGTCCCGCCCCATGGCCAATTCCACTCTCCTAGGGCTGCT  
GGCCCCGCCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCCCGAACCACAGCCCC  
CACCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTACTCCAACATCAAGACGGTG  
GCCCTGAACCTGCTCGTCACAGGAAGATTGTGGACCATGGCAATGGGACCTTCAGCGTCCACTT  
CCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCCTCGTGCCCCCAGTAAAGCTGTAG  
AGTTCCACCAGGAACAGCAGATCTTCATCGAAGCCAAGGCCTCCAAAATCTTCAACTGCCGGATG  
GAGTGGGAGAAGGTAGAACGGGGCCGCGGACCTCGCTTTGCACCCACGACCCAGCCAAGATCTG  
CTCCCGAGACCAGCTCAGAGCTCAGCCACCTGGAGCTGCTCCAGCCCTTCAAAGTCGTCTGTG  
TCTACATCGCCTTCTACAGCACGGACTATCGGCTGGTCCAGAAGGTGTGCCAGATTACAACACTAC  
CATAGTGATACCCCCTACTACCCATCTGGGTGACCCGGGGCAGGCCACAGAGGCCAGGCCAGGGC  
TGGAAGGACAGGCCTGCCATGCAGGAGACCATCTGGACACCGGGCAGGGAAGGGGTGGGCCTC  
AGGCAGGGAGGGGGTGGAGACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAG  
AGAAAGGGTCCCAAGTGCTGGTCCCAACCTGAAGCTGTGGAGTACTAGATCACAGGAGCACTGG  
AGGAGGAGTGGGCTCTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGG  
TCCCCGAGGCCTGTGGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGC  
CCTTGTTCTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGGAGATTTTCATCAGTGTGGACA  
GCCTGTCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAGGAGCCAGTCAGCAGGGTGGGGTGGG  
GCCAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCCTTGTCGTGTGCTGAGCATGG  
CATGAGGCTGAAGTGGCAACCCCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTCCAGC  
CAGGCCACCCCTTTCCAAAATTCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATTGCTGATG  
GCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCTCCACACTAAGGCCACAGCCCATC  
CGCGTGCTGTGTGTCCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAGCATCCATGTCCCG  
GAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTCAGACCGGGGTTCCTCCGGATCTGGATGGCGC  
CGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGCGGGCCGAGAGCATGTGCTGGATCTGTTT  
TGTGTGTCTGTCTGTGGGTGGGGGAGGGGAGGAAGTCTTGTGAAACCGCTGATTGCTGACTTT  
TGTGTGAAGAATCGTGTCTTGGAGCAGGAAATAAAGCTTGCCCCGGGGCA

## **FIGURE 92**

MQLTRCCFVFLVQGSILYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMANSTL  
LGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNGTF  
SVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMEWEKVERGRRTSLCTHDP  
AKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYRLVQKVC PDYNYHSDTPYYP SG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-14

**N-glycosylation sites.**

amino acids 62-65, 127-130, 137-140, 143-146

**2-oxo acid dehydrogenases acyltransferase**

amino acids 61-71



## FIGURE 93

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCCTGCGCTCGCC  
CTTTATGTCTTCACCATCGCCATCGAGCCGTGCGTATCATCTTCCTCATCGCCGGAGCTTCTT  
CTGGTTGGTGTCTCTACTGATTTCGTCCCTGTTTGGTTCATGGCAAGAGTCATTATTGACAACA  
AAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTGTCTATATCCAAGAA  
ATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTTGAAGAGTATAAACCC  
AGGTGAGACAGCACCCCTCTATGCGACTGCTGGCCTATGTTTCTGGCTTGGGCTTTGGAATCATGA  
GTGGAGTATTTTCCTTTGTGAATACCCTATCTGACTCCTTGGGGCCAGGCACAGTGGGCATTCAT  
GGAGATTCTCCTCAATTCTTCCTTTATTAGCTTTTCATGACGCTGGTCATTATCTTGCTGCATGT  
ATTCTGGGGCATTGTATTTTTTGTATGGCTGTGAGAAGAAAAGTGGGGCATCCTCCTTATCGTTC  
TCCTGACCCACCTGCTGGTGTGAGCCAGACCTTCATAAGTTCTTATTATGAATAAACCTGGCG  
TCAGCATTTATAATCCTGGTGTGCTGAGCCAGCTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCG  
AAGCCTGAAACTCTGCCTGCTCTGCCAAGACAAGAAGTTTCTTCTTTACAACCAGCGCTCCAGAT  
AACCTCAGGGAACCAGCACTTCCCAAACCGCAGACTACATCTTTAGAGGAAGCACAACTGTGCCT  
TTTTCTGAAAATCCCTTTTTCTGGTGGAATTGAGAAAGAAATAAACTATGCAGATA

## **FIGURE 94**

MTAAVFFGCAFIAFGPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDNKDG  
PTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGFGIMSGV  
FSFVNTLSDSLPGPTVGIHGDSPOFFLYSAFMTLVIILLHVFWGIVFFDGCEKKKWGILLIVLLT  
HLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLKLCCLLCQDKNFLLYNQRSR

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**Transmembrane domains:**

amino acids 32-51, 119-138, 152-169, 216-235

**Glycosaminoglycan attachment site.**

amino acids 120-123

**Sodium:neurotransmitter symporter family protein**

amino acids 31-65

## FIGURE 95

AATTTTTCACCAGAGTAAACTTGAGAAACCAACTGGACCTTGAGTATTGTACATTTTGCCTCGTG  
GACCCAAAGGTAGCAATCTGAAACATGAGGAGTACGATTCTACTGTTTTGTCTTCTAGGATCAAC  
TCGGTCATTACCACAGCTCAAACCTGCCTTGGGACTCCCTCCCACAAAACCTGGCTCCGGATCAGG  
GAACACTACCAAACCAACAGCAGTCAAATCAGGTCTTTCCTTCTTTAAGTCTGATACCATTAACA  
CAGATGCTCACACTGGGGCCAGATCTGCATCTGTAAATCCTGCTGCAGGAATGACACCTGGTAC  
CCAGACCCACCCATTGACCTGGGAGGGTTGAATGTACAACAGCAACTGCACCCACATGTGTTAC  
CAATTTTGTACACAACCTGGAGCCCAGGGCACTATCCTAAGCTCAGAGGAATTGCCACAAATC  
TTCACGAGCCTCATCATCCATTCTTGTTCCTGGGAGGCATCCTGCCACCAGTCAGGCAGGGGC  
TAATCCAGATGTCCAGGATGGAAGCCTTCCAGCAGGAGGAGCAGGTGTAAATCCTGCCACCCAGG  
GAACCCAGCAGGCCGCCTCCCAACTCCCACTGGCAGATGACGACTTTGCAGTGACCAACCCCT  
GCAGGCATCCAAAGGAGCACACATGCCATCGAGGAAGCCACCACAGAATCAGCAAATGGAATTCA  
GTAAGCTGTTTCAAATTTTTTCAACTAAGCTGCCTCGAATTTGGTGATACATGTGAATCTTTATC  
ATTGATTATATTATGGAATAGATTGAGACACATTGGATAGTCTTAGAAGAAATTAATTCTTAATT  
TACCTGAAATATTCTTGAAATTTAGAAATATGTTCTATGTAGAGAATCCCAACTTTTAAAAA  
CAATAATTCAATGGATAAATCTGTCTTTGAAATATAACATTATGCTGCCTGGATGATATGCATAT  
TAAACATATTTGAAAACCTGGAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 96**

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSLSLIPLTQM  
LTILGPDHLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPFI FVTQLGAQG TILSSEE  
LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGS LPAGGAGVNPATQGT PAGRLPTPSG  
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

**Signal peptide:**

amino acids 1-16

## FIGURE 97

GCTCAAGTGCCCTGCCTTGCCCCACCCAGCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGCTCT  
CTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGGCGCTGGAGGGCCTGTCCTGACCATG  
GTCCCTGCCTGGCTGTGGCTGCTTTGTGTCTCCGTCCCCAGGCTCTCCCAAGGCCAGCCTGC  
AGAGCTGTCTGTGGAAGTTCCAGAAACTATGGTGGAAATTTCCCTTTATACCTGACCAAGTTGC  
CGCTGCCCCGTGAGGGGGCTGAAGGCCAGATCGTGTGTGAGGGGACTCAGGCAAGGCAACTGAG  
GGCCCATTTGCTATGGATCCAGATTCTGGCTTCTGTGGTGACAGGGCCCTGGACCCGAGAGGA  
GCAGGCAGAGTACCAGCTACAGGTACCCCTGGAGATGCAGGATGGACATGTCTTGTGGGGTCCAC  
AGCCTGTGCTTGTGCACGTGAAGGATGAGAATGACCAGGTGCCCCATTTCTCTCAAGCCATCTAC  
AGAGCTCGGCTGAGCCGGGTACCAGGCTGGCATCCCTTCTCTTCTTGGGCTTCAGACCG  
GGATGAGCCAGGCACAGCCAACTCGGATCTTCGATTCCACATCCTGAGCCAGGCTCCAGCCCAGC  
CTTCCCCAGACATGTTCCAGCTGGAGCCTCGGCTGGGGCTCTGGCCCTCAGCCCCAAGGGGAGC  
ACCAGCCTTGACCACGCCCTGGAGAGGACCTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGA  
CCAGGCCCTCAGGCCACCCAGCCACTGCCACCGTGGAAAGTCTCCATCATAGAGAGCAGCTGGGTGT  
CCCTAGAGCCTATCCACCTGGCAGAGAATCTCAAAGTCTATACCCGCACCACATGGCCCCAGGTA  
CACTGGAGTGGGGGTGATGTGCACTATCACCTGGAGAGCCATCCCCGGGACCCCTTGAAGTGAA  
TGCAGAGGGAAACCTCTACGTGACCAGAGAGCTGGACAGAGAAGCCAGGCTGAGTACCTGCTCC  
AGGTGCGGGCTCAGAATTCCTATGGCGAGGACTATGCGGCCCTCTGGAGCTGCACGTGCTGGTG  
ATGGATGAGAATGACAACGTGCCTATCTGCCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCT  
CAGTCCACCAGGTACTGAAGTGACTAGACTGTGACAGAGGATGCAGATGCCCCGGCTCCCCCA  
ATTCCCACGTTGTGTATCAGCTCCTGAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCTTC  
CAGGTGGACCCCACTTCAGGCAGTGTGACGCTGGGGGTGCTCCCACTCCGAGCAGGCCAGAACAT  
CCTGCTTCTGGTGCTGGCCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCAGTGTGAAG  
TCGAAGTCGCAGTCACAGATATCAATGATCACGCCCCCTGAGTTCATCACTTCCCAGATTGGGCC  
ATAAGCCTCCCTGAGGATGTGGAGCCCGGACTCTGGTGGCCATGCTAACAGCCATTGATGCTGA  
CCTCGAGCCCGCCTTCCGCCCTCATGGATTTGCCATTGAGAGGGGAGACACAGAAGGGACTTTTG  
GCCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAAGAACCTCAGTTATGAG  
GCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGAAGCTGGTGGGGCCAGGCC  
AGGCCCTGGAGCCACCGCCACGGTGACTGTGCTAGTGGAGAGAGTGTGCCACCCCCAAGTTGG  
ACCAGGAGAGCTACGAGGCCAGTGTCCCCATCAGTGGCCAGCCGGCTCTTCTGCTGACCATC  
CAGCCCTCCGACCCCATCAGCCGAACCCCTCAGGTTCTCCCTAGTCAATGACTCAGAGGGCTGGCT  
CTGCATTGAGAAATTTCTCCGGGGAGGTGCACACCGCCAGTCCCTGCAGGGCGCCAGCCTGGGG  
ACACCTACACGGTGCTTGTGGAGGGCCAGGATACAGCCCTGACTCTTGCCCCGTGTCCTCCCCA  
TACCTCTGCACACCCCGCCAGACCATGGCTTGATCGTGAGTGGACCCAGCAAGGACCCCGATCT  
GGCCAGTGGGCACGGTCCCTACAGCTTACCCCTTGGTCCCAACCCACGGTGCAACGGGATTGGC  
GCCTCCAGACTCTCAATGGTTCCCATGCCATACCTACCTTGGCCCTGCATTGGGTGGAGCCACGT  
GAACACATAATCCCGTGGTGGTGCAGCCACAATGCCAGATGTGGCAGCTCCTGGTTTCAGTGAT  
CGTGTGTGCTGCAACGTGGAGGGGAGTGCATGCGCAAGGTGGGCCGATGAAGGGCATGCCCA  
CGAAGCTGTGGCAGTGGGCATCCTTGTAGGCACCCCTGGTAGCAATAGGAATCTTCTCATCCTC  
ATTTTACCCACTGGACCATGTCAAGGAAGAAGGACCCGATCAACCAGCAGACAGCGTGGCCCT  
GAAGGCGACTGTCTGAATGGCCAGGCAGCTCTAGCTGGGAGCTTGGCTCTGGCTCCATCTGAG  
TCCCTGGGAGAGAGCCAGCACCCAAAGATCCAGCAGGGGACAGGACAGAGTAGAAGCCCTCCA  
TCTGCCCTGGGGTGGAGGCACCATCACCATCACCAGGCATGTCTGCAGAGCCTGGACCAACTT  
TATGGAAGTGGCCATGGGAGTGTCCAAATGTCAGGGTGTGTGCCCAATAATAAAGCCCCAGAGAA  
CTGGGCTGGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG

## **FIGURE 98**

MVPAWLWLLCVSPQALPKAQAELSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSGKAT  
EGPFAMDPDSGFLLVTRALDREEQAEYQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVPHFSQAI  
YRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQSPDMFQLEPRLGALALSPKG  
STSLDHALERTYQLLVQVKMDQASGHQATATVEVSIESTWVSLEPIHLAENLKVLYPHMAQ  
VHWSGGDVHYHLESHPPGPFVNAEGNLYVTRELDREAQAEYLLQVRAQNSHGEDIAAPLELHVL  
VMDENDNVPICPPRPDPTVSIPELSPPGTEVTRLAEDADAPGSPNSHVYQLLSPEPEDGVEGRA  
FQVDPTSGSVTLGVLPLRAGQNILLVLAMDLAGAEGGFSSTCEVEVAVTDINDHAPEFITSQIG  
PISLPEDVEPGTLVAMLTADADLEPAFRLMDFAIERGDTEGTFGLDWEPPDSGHVRLRLCKNLSY  
EAAPSHEVVVVVQSVAKLVGPGPGGATATVTVLVERVMPPPKLDQESYEASVPISAPAGSFLLT  
IQPSDPISRTRLRFSLVNDSEGWLCEKFSGEVHTAQSLQGAQPGDTYTVLVEAQDTALTLPVPS  
QYLCTPRQDHGLIVSGPSKDPDLASGHGPYSFTLGPNPTVQRDWRLQTLNGSHAYLTLALHWVEP  
REHIIPVVVSHNAQMQLLVRVIVCRCNVEGQCMRKVGRMKGMPTKLSAVGILVGTIVAIGIFLI  
LIFTHWTMSRKKDPDQPADSVPLKATV

### **Signal peptide:**

amino acids 1-18

### **Transmembrane domain:**

amino acids 762-784

## FIGURE 99

GGCTGACCGTGCTACATTGCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGCTGCCCACGCCTG  
AGTCCAAGATTCTTCCCAGGAACACAAACGTAGGAGACCCACGCTCCTGGAAGCACCAGCCTTTA  
TCTCTTCACCTTCAAGTCCCCTTTCTCAAGAATCCTCTGTTCTTTGCCCTCTAAAGTCTTGGTAC  
ATCTAGGACCCAGGCATCTTGCTTTCCAGCCACAAAGAGACAGATGAAGATGCAGAAAGGAAATG  
TTCTCCTTATGTTTGGTCTACTATTGCATTTAGAAGCTGCAACAAATCCAATGAGACTAGCACC  
TCTGCCAACACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGCCACCAACTCTGGGTCCAG  
TGTGACCTCCAGTGGGGTCAGCACAGCCACCATCTCAGGGTCCAGCGTGACCTCCAATGGGGTCA  
GCATAGTCACCAACTCTGAGTTCCATAACAACCTCCAGTGGGATCAGCACAGCCACCAACTCTGAG  
TTCAGCACAGCGTCCAGTGGGATCAGCATAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGG  
GGCCAGCACAGCCACCAACTCTGAGTCCAGCACACCCTCCAGTGGGGCCAGCACAGTCCACCAACT  
CTGGGTCCAGTGTGACCTCCAGTGGAGCCAGCACTGCCACCAACTCTGAGTCCAGCACAGTGTCC  
AGTAGGGCCAGCACTGCCACCAACTCTGAGTCTAGCACACTCTCCAGTGGGGCCAGCACAGCCAC  
CAACTCTGACTCCAGCACAACTCCAGTGGGGCTAGCACAGCCACCAACTCTGAGTCCAGCACAA  
CTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACT  
GCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAG  
AACGACCTCCAATGGGGCTGGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGGCCA  
GCACAGCCACCAACTCTGACTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAG  
TCCAGCACGACCTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGG  
GGCTAGCACAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCGGCACAGCCACCAACT  
CTGAGTCCAGCACAGTGTCCAGTGGGATCAGCACAGTCAACCAATTCTGAGTCCAGCACACCCTCC  
AGTGGGGCCAACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGGGGCCAACACAGCCAC  
CAACTCTGAGTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACAA  
CCTCCAGTGGGGTCAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCTAGCACAA  
GCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCTAG  
CACAGTGTCCAGTGGGATCAGCACAGTCAACCAATTCTGAGTCCAGCACAACTCCAGTGGGGCCA  
ACACAGCCACCAACTCTGGGTCCAGTGTGACCTCTGCAGGCTCTGGAACAGCAGCTCTGACTGGA  
ATGCACACAACCTCCCATAGTGCATCTACTGCAGTGTGAGGCAAAGCCTGGTGGGTCCCTGGT  
GCCGTGGGAAATCTTCTCATCACCTGGTCTCGGTTGTGGCGGCCGTGGGGCTCTTTGCTGGGC  
TCTTCTTCTGTGTGAGAAACAGCCTGTCCCTGAGAAACACCTTTAACACAGCTGTCTACCACCT  
CATGGCCTCAACCATGGCCTTGGTCCAGGCCCTGGAGGGAATCATGGAGCCCCCAGAGGCCAG  
GTGGAGTCTTAAGTGGTCTGGAGGAGACCAAGTATCATCGATAGCCATGGAGATGAGCGGGAGGA  
ACAGCGGGCCCTGAGCAGCCCCGGAAGCAAGTGCCGCATTCTTCAGGAAGGAAGAGACCTGGGCA  
CCCAAGACCTGGTTTCTTTTCATTTCATCCAGGAGACCCCTCCAGCTTTGTTTGAGATCCTGAA  
AATCTTGAAGAAGGTATTCTTCACCTTTCTTGCTTTTACCAGACACTGGAAAGAGAATACTATAT  
TGCTCATTTAGCTAAGAAATAAATACATCTCATCTAACACACACGACAAAGAGAAGCTGTGCTTG  
CCCCGGGGTGGGTATCTAGCTCTGAGATGAAGTCAAGTTATAGGAGAAAACCTCCATGCTGGACTC  
CATCTGGCATTCAAAATCTCCACAGTAAATCCAAAGACCTCAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 100**

MRMQKGNVLLMFGLLLHLEAATNSNETSTSANTGSSVISSGASTATNSGSSVTSSGVSTATISGS  
SVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSESSTPSS  
GASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSSTTSSGASTA  
TNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTTSNGAGTATNSES  
STTSSGASTATNSDSSTVSSGASTATNSESSTTSSGASTATNSESSTTSSGASTATNSDSSTTSS  
GAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGANTATNSESSTVSSGASTA  
TNSESSTTSSGVSTATNSESSTTSSGASTATNSDSSTTSSEASTATNSESSTVSSGISTVTNSES  
STTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAVSEAKPGGSLVPWEI FLITLVSVVA  
AVGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGPGPGGNHGAPHRPRWSPNWFWRPVS I  
AMEMSGRNSGP

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 510-532



## FIGURE 101

GGCCGGACGCTCCGCGTTACGGGATGAATTAACGGCGGGTTCCGCACGGAGGTTGTGACCCCTA  
CGGAGCCCCAGCTTGCCACGCACCCCACTCGGCGTCGCGCGGCGTGCCCTGCTTGTCACAGGTG  
GGAGGCTGGAACTATCAGGCTGAAAAACAGAGTGGGTACTCTCTTCTGGGAAGCTGGCAACAAAT  
GGATGATGTGATATATGCATTCCAGGGGAAGGGAATTTGGTGTCTCTGAACCCATGGTCAATT  
AACGAGGCAGTTTCTAGCTACTGCACGTACTTCATAAAGCAGGACTCTAAAAGCTTTGGAATCAT  
GGTGTGATGGAAAGGATTTACTTTTACTGACTCTGTTTTGGGGAAGCTTTTTTGAAGCATT  
TCATGCTGAGTCCCTTTTTACCTTTGATGTTTGTAACCCATCTTGGTATCGCTGGATCAACAAC  
CGCCTTGTTGGCAACATGGCTCACCTACCTGTGGCATTATTGGAGACCATGTTTGGTGTAAAAGT  
GATTATAACTGGGGATGCATTGTTCTGGAGAAAGAAGTGTATTATCATGAACCATCGGACAA  
GAATGGACTGGATGTTCTGTGGAATTGCCTGATGCGATATAGCTACCTCAGATTGGAGAAAATT  
TGCTCAAAGCGAGTCTCAAAGGTGTTCTCGATTGTTGGTGGGCCATGCAGGCTGCTGCCTATAT  
CTTCATTATAGGAAATGGAAGGATGACAAGAGCCATTTGAAGACATGATTGATTACTTTTGTG  
ATATTCACGAACCACTTCAACTCCTCATATTCCCAGAAGGGACTGATCTCACAGAAAACAGCAAG  
TCTCGAAGTAATGCATTTGCTGAAAAAATGGACTTCAGAAATATGAATATGTTTTACATCCAAG  
AACTACAGGCTTTACTTTTTGTGGTAGACCGTCTAAGAGAAGGTAAGAACCTTGATGCTGTCCATG  
ATATCACTGTGGCGTATCCTCACAACTTCTCAATCAGAGAAGCACCTCCTCCAAGGAGACTTT  
CCCAGGGAAATCCACTTTACAGTCCACCGGTATCCAATAGACACCTCCCCACATCCAAGGAGGA  
CCTTCAACTCTGGTGCCACAAACGGTGGGAAGAGAAAGAAGAGAGGCTGCGTTCCTTCTATCAAG  
GGGAGAAGAATTTTATTTTACCGGACAGAGTGTATTCCACCTTGCAAGTCTGAACTCAGGGTC  
CTTGTGGTCAAATTGCTCTCTATACTGTATTGGACCCTGTTTCAGCCCTGCAATGTGCCTACTCAT  
ATATTTGTACAGTCTTGTTAAGTGGTATTTTATAATCACCATTGTAATCTTTGTGCTGCAAGAGA  
GAATATTTGGTGGACTGGAGATCATAGAACTTGCATGTTACCGACTTTTACACAAACAGCCACAT  
TTAAATTCAAAGAAAAATGAGTAAGATTATAAGGTTTGCCATGTGAAAACCTAGAGCATATTTTG  
GAAATGTTCTAAACCTTTCTAAGCTCAGATGCATTTTTGCATGACTATGTGCAATATTTCTTACT  
GCCATCATTATTTGTAAAGATATTTTGCATTAATTTTGTGGGAAAAATATTGCTACAATTTTT  
TTAATCTCTGAATGTAATTTGATACTGTGTACATAGCAGGGAGTGATCGGGGTGAAATAACTT  
GGCCAGAATATTATTAAACAATCATCAGGCTTTTAAA

## **FIGURE 102**

MHSRGREIVVLLNPWSINEAVSSYCTYFIKQDSKSGIMVSWKGIYFILTLFWGSFFGSIIFMLSP  
FLPLMFVNPSWYRWINNRLVATWLTLPVALLETMFGVKVIITGDAFVPGERSVIIMNHRTRMDWM  
FLWNCLMRYSYLRLEKICKASLKGVPFGWAMQAAAYIFIHRKWKDDKSHFEDMIDYFCDIHEP  
LQLLIFPEGTDLTENSRSNAFAEKNGLQKYEYVLHPRTTGFTFVVDRLREGKNLDAVHDITVA  
YPHNIPQSEKHLQGDFFREIHFHVHRYPIDTLPTSKEDLQLWCHKRWEEKEERLRSFYQGEKNF  
YFTGQSVIPPCKSELRLVLVKKLSILYWTLFSPAMCLLIYLYSLVKWYFIITIVIFVLQERIFGG  
LEIIEIACRYRLLHKQPHLNSKKNE

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**Transmembrane domains:**

amino acids 44-63, 90-108, 354-377

## **FIGURE 103**

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTGACC  
TCCAAATCATCCATCCACCCCTGCTGTCTATCTGTTTTCATAGTGTGAGATCAACCCACAGGAATA  
TCCATGGCTTTTGTGCTCATTTTGGTTCTCAGTTTTCTACGAGCTGGTGTGAGGACAGTGGCAAGT  
CACTGGACCGGGCAAGTTTGTCCAGGCCTTGGTGGGGGAGGACGCCGTGTTCTCCTGCTCCCTCT  
TTCCTGAGACCAGTGCAGAGGCTATGGAAGTGCAGTTCTTCAGGAATCAGTTCCATGCTGTGGTC  
CACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACAGTATCGAGGGAGAATGA  
GTTTGTGAAGGACTCCATTGCAGGGGGCGTGTCTCTCTAAGGCTAAAAACATCACTCCCTCGG  
ACATCGGCCTGTATGGGTGCTGGTTCAGTTCCCAGATTACGATGAGGAGGCCACCTGGGAGCTG  
CGGGTGGCAGCACTGGGCTCACTTCCTCTCATTTCCATCGTGGGATATGTTGACGAGGTATCCA  
GTTACTCTGCCTGTCTCAGGCTGGTTCCCCCAGCCACAGCCAAGTGGAAAGGTCCACAAGGAC  
AGGATTTGTCTTCAGACTCCAGAGCAAATGCAGATGGGTACAGCCTGTATGATGTGGAGATCTCC  
ATTATAGTCCAGGAAAATGCTGGGAGCATATTGTGTTCCATCCACCTTGCTGAGCAGAGTCATGA  
GGTGAATCCAAAGGTATTGTAGGAGAGACGTTTTTCCAGCCCTCACCTTGGCGCCTGGCTTCTA  
TTTTACTCGGGTTACTCTGTGTGCTGCTGTGTGTTGTGTCATGGGGATGATAATTGTTTTCTTC  
AAATCCAAAGGAAAATCCAGGCGGAACCTGGACTGGAGAAGAAAGCACGGACAGGCAGAATTGAG  
AGACGCCCGGAAACACGCAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAGCTCTGCG  
TTTCTGATCTGAAAACCTGTAACCCATAGAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGA  
TTTACAAGGAAGAGTGTGGTGGCTTCTCAGGGTTTCCAGCAGGGAGACATTACTGGGAGGTGGA  
CGTGGGACAAAATGTAGGGTGGTATGTGGGAGTGTGTGCGGATGACGTAGACAGGGGGAAGAACA  
ATGTGACTTTTGTCTCCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTTGTATTTCT  
ACATTCATCCCATTTTATCAGCCTCCCCCAGCACCCCTCCTACACGAGTAGGGGTCTTCCT  
GGACTATGAGGGTGGGACCATCTCCTTCTTCAATAACAATGACCAGTCCCTTATTTATACCCTGC  
TGACATGTCTAGTTTGAAGGCTTGTGAGACCTATATCCAGCATGCGATGTATGACGAGGAAAAG  
GGGACTCCCATATTATATGTCCAGTGTCTCGGGATGAGACAGAGAAGACCCTGCTTAAAGGGC  
CCCACACCACAGACCCAGACACAGCCAAGGGAGAGTGTCTCCGACAGGTGGCCCCAGCTTCTCT  
CCGGAGCCTGCGCACAGAGAGTCACGCCCCCACTCTCCTTTAGGGAGCTGAGGTTCTTCTGCCC  
TGAGCCCTGCAGCAGCGGCAGTCACAGCTTCCAGATGAGGGGGGATTGGCCTGACCCTGTGGGAG  
TCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCACATTAGGTTTAGTTTGTGAAAA  
CTCCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCCAGGCTCCTCATTTGCTAGTCACGG  
ACAGTGATTCTGCTCACAGGTGAAGATTAAAGAGACAACGAATGTGAATCATGCTTGCAGGTT  
TGAGGGCACAGTGTGCTAATGATGTGTTTTATATTATACATTTTCCCACCATAAACTCTGTT  
TGCTTATTCACATTAATTTACTTTTCTCTATACCAAATCACCCATGGAATAGTTATTGAACACC  
TGCTTTGTGAGGCTCAAAGAATAAAGAGGAGGTAGGATTTTCACTGATTCTATAAGCCAGCAT  
TACCTGATACCAAAACCAGGCAAGAAAACAGAGAAGAGGAAGGAAAACCTACAGGTCCATATCC  
CTCATTAACACAGACACAAAAATCTAAATAAAATTTTAAACAAATTAACATAAACAATATATTTA  
AAGATGATATATACTACTCAGTGTGGTTTTGTCCACAAATGCAGAGTTGGTTTAATATTTAAAT  
ATCAACCAGTGTAATTCAGCACATTAATAAAGTAAAAAAGAAAACCATAAAAA

## **FIGURE 104**

MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHAVVH  
LYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEEATWELR  
VAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGYSLYDVEISI  
IVQENAGSILCSIHLAEQSHEVESKVLIGETFFQPSPWRLASILLGLLCGALCGVVMGMIIVFFK  
SKGKIQAELDWRRKHGQAEIRDARKHAVEVTLDPETAHPKLCVSDLKTVTHRKAQEVPHSEKRF  
TRKSVVASQGFQAGRHYEVDVGQNVGWYVGVCRDDVDRGKNNVTLSPNNGYWVLRLTTEHLYFT  
FNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLLTCQFEGLLRPYIQHAMYDEEKG  
TPIFICPVSWG

### **Signal peptide:**

amino acids 1-17

### **Transmembrane domains:**

amino acids 131-150, 235-259

## FIGURE 105

CCTTCACAGGACTCTTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTAGGAAAAGAG  
TTTGTGGGAACCCCTGGGTTATCGGCCTCGTCATCTTCATATCCCTGATTGTCCTGGCAGTGTGCATTGGA  
CTCACTGTTTCATTATGTGAGATATAATCAAAGAAGACCTACAATTACTATAGCACATTGTCATTTACAAC  
TGACAAACTATATGCTGAGTTTGGCAGAGAGGCTTCTAACAATTTTACAGAAATCAGCCAGAGACTTGAAT  
CAATGGTGAAAAATGCATTTTATAAATCTCCATTAAGGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTC  
AGTCAACAGAAGCATGGAGTGTGGCTCATATGCTGTTGATTTGTAGATTTCACTCTACTGAGGATCCTGA  
AACTGTAGATAAAATTTGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTAG  
ATCCTCACTCAGTTAAAATTAAAAAATCAACAAGACAGAAACAGACAGCTATCTAAACCATTGCTGCGGA  
ACACGAAGAAGTAAACTCTAGGTGAGGTCTCAGGATCGTTGGTGGGACAGAAGTAGAAGAGGGTGAATG  
GCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGTGGAGCAACCTTAATTAATGCCACATGGC  
TTGTGAGTGCTGCTCACTGTTTACAACATATAAGAACCCTGCCAGATGGACTGCTTCCCTTTGGAGTAACA  
ATAAACCTTCGAAAATGAAACGGGGTCTCCGGAGAATAATTGTCCATGAAAAATACAAACACCCATCACA  
TGACTATGATATTTCTCTGCAGAGCTTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCT  
TCCCTGATGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAAAT  
GATGTTTACAGTCAAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAACCTGCAATGAACC  
TCAAGCTTACATGACGCCATACTCCTAGAATGTTATGTGCTGGCTCCTTAGAAGGAAAAACAGATGCAT  
GCCAGGGTGACTCTGGAGGACCACTGGTTAGTTCAGATGCTAGAGATATCTGGTACCTTGCTGGAATAGTG  
AGCTGGGGAGATGAATGTGCGAAACCAACAAGCCTGGTGTCTTACTAGAGTTACGGCCTTGCGGGACTG  
GATTACTTCAAAAACCTGGTATCTAAGAGACAAAAGCCTCATGGAACAGATAACATTTTTTTTTTGTTTTTTG  
GGTGTGGAGGCCATTTTATAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTTGACTGATCTCA  
ATAAACTGTTTGCTTGATGCATGTATTTCTTCCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTGCCA  
GATCAACTCTGTATCTGTGAGCAATAGTTGAAACTTTATGTACATAGAGAAATAGATAATACAATATTAC  
ATTACAGCCTGTATTCATTTGTTCTCTAGAAGTTTGTGAGAATTTTGACTTGTGACATAAATTTGTAAT  
GCATATATACAATTTGAAGCACTCCTTTCTTCAGTTCCTCAGCTCCTCTCATTTCAGCAAATATCCATTT  
TCAAGGTGCAGAACAGGAGTGAAAGAAAATATAAGAAGAAAAAATCCCTACATTTTATTGGCACAGAA  
AAGTATTAGGTGTTTTCTTAGTGAATATTAGAAATGATCATATTATTATGAAAGGTCAAGCAAAGACA  
GCAGAATACCAATCACTTCATCATTTAGGAAGTATGGGAACTAAGTTAAGGAAGTCCAGAAAGAAGCCAAG  
ATATATCCTTATTTTCAATTCAAAACAACTACTATGATAAATGTGAAGAAGATTCTGTTTTTTTGTGACCT  
ATAATAATTATACAAACTTCATGCAATGTACTTGTCTAAGCAAATTAAAGCAAATATTTATTAACATTG  
TTACTGAGGATGTCAACATATAACAATAAAATATAAATCACCCA

## **FIGURE 106**

MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYYSTLSFTTDKLY  
AEFGREASNNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSQQKHGVLAHMLLICRFHSTED  
PETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTLGQSLRIVGG  
TEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAHCFTTYKNPARWTASFGVTIKPSKMKRGL  
RRIIVHEKYKHPSHDYDISLAELSSPVPTNAVHRVCLPDASYEFQPGDVMFVTGFGALKNDGYS  
QNHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGDSSGGLVSSDARDIWYLAG  
IVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

**Transmembrane domain:**

amino acids 21-40 (type II)

## FIGURE 107

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCCCTG  
CCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCACCAGGGCCCAGC  
GCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGATGGGGCTTCTCCCTT  
ACGGGGGCTCACAATGGCCCAGAGAAGATTCCGTGAAGTGCTGCGCTGCCTGCTCTACGCCCTCAA  
TCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGATGAGGGACTACCTAA  
ATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTCATTTGACTTACTTTCCT  
GTGGTTTCATCCGGTCATGATTGCTGTTTCTGTTTCTTATCATTGTGGGATGTTAGGATATTG  
TGAACGGTGAAAAGAAATCTGTTGCTTCTTGCATGGTACTTTGGAAGTTTGCTGTCTATTTCT  
GTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAGGAACCTATGGTTCCAGTACAATGGTCA  
GATATGGTCACTTTGAAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCA  
TGCTTGGAAATTTTTTTCAGAGAGAGTTTAAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTG  
AAATGACAGAGATGGACTGGCCCCAGATTCTGCTGTGTTAGAGAATTTCCAGGATGTTCCAAA  
CAGGCCCCACGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTATTCCCTT  
TTTGAGAGGAACCAACAACACTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAAA  
TCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCTGGG  
ACAGACCAATGATGTCCTTGAAGAATGACAACCTCTCAGCACCTGTCATGTCCCTCAGTAGAACT  
GTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCCATGGCAAACAGCTTTAATACACACT  
TTGAGATGGAGGAGTTATAAAAAGAAATGTCACAGAAGAAAACCAAACTTGTTTTATTGGACT  
TGTGAATTTTTGAGTACATACTATGTGTTTCAGAAATATGTAGAAATAAAAATGTTGCCATAAAA  
TAACACCTAAGCATATACTATTCTATGCTTTAAATGAGGATGGAAAAGTTTCATGTCATAAGTC  
ACCACCTGGACAATAATTGATGCCCTTAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCC  
TGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCA  
TCCATGCAAACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGTTGATTTACTTCTACCAA  
CTAGTATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA  
CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACCTTTCAATATTGGTGACT  
ACCTAAATGTGATTTTTGCTGGTTACTAAATATTCTTACCACTTAAAGAGCAAGCTAACACAT  
TGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTGTATAATTTCAGTCGAT  
TTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAATTTGTCCTGTATAGCATCATT  
ATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGTCCTGGGCTTATATTACACATATAAC  
TGTTATTTAAATACTTAACCACTAATTTTGAAAATTACCACTGTGATACATAGGAATCATTATTC  
AGAATGTAGTCTGGTCTTTAGGAAGTATTAATAAGAAAATTTGCACATAACTTAGTTGATTGAGA  
AAGGACTTGTATGCTGTTTTCTCCAAATGAAGACTCTTTTGGACACTAAACACTTTTAAAAA  
GCTTATCTTTGCCTTCTCCAAACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAA  
TAGTGTTCTTTTCTCCAGAAAAATGCTTGTGAGAATCATTAACATGTGACAATTTAGAGATT  
CTTTGTTTTATTTCAGTGATTAATATACTGTGGCAAATTACACAGATTATTAATTTTTTACAA  
GAGTATAGTATATTTATTTGAAATGGGAAAAGTGCAATTTTACTGTATTTTGTGATTTTGTATTAT  
TTCTCAGAATATGGAAGAAAATTAAATGTGTCAATAAATATTTTCTAGAGAGTAA

## **FIGURE 108**

MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAE TRVEEAVILTYFPVVHP  
VMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQWSDMVT  
LKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTMDWPPDSCCVREFPGCSKQAHQ  
EDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWALYYDRREP GTDQM  
MSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

### **Signal peptide:**

amino acids 1-33

### **Transmembrane domains:**

amino acids 12-35, 57-86, 94-114, 226-248



## FIGURE 109

CCAAGGCCAGAGCTGTGGACACCTTATCCCACTCATCCTCATCCTCTTCCTCTGATAAAGCCCTACCAGTGCT  
 GATAAAGTCTTTCTCGTGAGAGCCTAGAGGCCTTAAAAAAAAGTGCTTGAAAGAGAAGGGGACAAAGGAACA  
 CCAGTATTAAGAGGATTTTCCAGTGTTCTGGCAGTTGGTCCAGAAGGATGCTCCATTCCTGCTTCTCACCTG  
 CCTCTTCATCACAGGCACCTCCGTGTCACCCGTGGCCCTAGATCCTTGTCTGCTTACATCAGCCTGAATGAGC  
 CCTGGAGGAACACTGACCACCACTTGGATGAGTCTCAAGGTCCTCCTCTATGTGACAACCATGTGAATGGGGAG  
 TGGTACCACCTTCACGGGCATGGCGGGAGATGCCATGCCTACCTTCTGCATACCAGAAAACCACTGTGGAACCCA  
 CGCACCTGTCTGGCTCAATGGCAGCCACCCCTAGAAAGGCGACGGCATTGTGCAACGCCAGGCTTGTGCCAGCT  
 TCAATGGGAACCTGCTGTCTCTGGAACACCACGGTGGAACTCAAGGCTTGCCTTGAGGGCTACTATGTGTATCGT  
 CTGACCAAGCCAGCGTCTGCTTCCACGTCTACTGTGGTCATTTTTATGACATCTGCGACGAGGACTGCCATGG  
 CAGCTGCTCAGATACCAGCGAGTGCACATGCCCTCCAGAACTGTGCTAGGCCCTGACAGGCAGACATGCTTTG  
 ATGAAAATGAATGTGAGCAAAACAACGGTGGCTGCAGTGAGATCTGTGTGAACCTCAAAAACCTCTACCGCTGT  
 GAGTGTGGGGTGGCCGTGTGCTAAGAAGTGATGGCAAGACTTGTGAAGACGTTGAAGGATGCCACAATAACAA  
 TGGTGGCTGCAGCCACTCTTGCTTGGATCTGAGAAAGGCTACCAGTGTGAATGTCCCCGGGGCCTGGTGCTGT  
 CTGAGGATAACCACACTTGCCAAGTCCCTGTGTTGTGCAAAATCAAATGCCATTGAAGTGAACATCCCCAGGGAG  
 CTGGTTGGTGGCCTGGAGCTCTTCTGACCAACACCTCCTGCCGAGGAGTGTCCAACGGCACCCATGTCAACAT  
 CCTCTTCTCTCAAGACATGTGGTACAGTGGTCGATGTGGTGAATGACAAGATTGTGGCCAGCAACCTCGTGA  
 CAGGTCTACCAAGCAGACCCCGGGGAGCAGCGGGGACTTCATCATCCGAACCAGCAAGCTGCTGATCCCGGTG  
 ACCTGCGAGTTTCCACGCCGTGTACACCATTTCTGAAGGATACGTTCCCAACCTTCGAAACTCCCCACTGGAAT  
 CATGAGCCGAAATCATGGGATCTTCCCATTCACTCTGGAGATCTTCAAGGACAATGAGTTTGAAGAGCCTTACC  
 GGGAAGCTCTGCCCACCCTCAAGCTTCGTGACTCCCTCTACTTTGGCATTGAGCCCGTGGTGACGTGAGCGGC  
 TTGGAAGCTTGGTGAGAGCTGCTTTGCCACCCCACTCCAAGATCGACGAGGTCCTGAAATACTACCTCAT  
 CCGGGATGGCTGTGTTTCAGATGACTCGGTAAAGCAGTACACATCCCGGGATCACCTAGCAAAGCACTTCCAGG  
 TCCCTGTCTTCAAGTTTGTGGGCAAAGACCACAAGGAAGTGTCTGCACTGCCGGGTCTTGTCTGTGGAGTG  
 TTGGACGAGCGTTCCCGCTGTGCCAGGGTTGCCACCGCGAATGCGTCTGGGGCAGGAGGAGAGGACTCAGC  
 CGGTCTACAGGGCCAGACGCTAACAGGCGGCCGATCCGCATCGACTGGGAGGACTAGTTCGTAGCCATACCTC  
 GAGTCCCTGCATTGGACGGCTCTGCTCTTTGGAGCTTCTCCCCCACC GCCCTCTAAGAACATCTGCCAACAGC  
 TGGGTTCCAGACTTCACACTGTGAGTTCAGACTCCAGCACCACTCACTCTGATTCTGGTCCATTCACTGGGCA  
 CAGGTACAGCACTGCTGAACAATGTGGCTGGGTGGGTTTCATCTTTCTAGGTTGAAAACCTAACTGTCCA  
 CCCAGAAAGACACTCACCCATTTCCCTCATTTCTTCTTACACTTAAATACCTCGTGTATGGTGCAATCAGAC  
 CACAAAATCAGAAGCTGGGTATAATATTTCAAGTTACAAACCCTAGAAAAATTAAACAGTTACTGAAATTATGA  
 CTAAATACCAATGACTCCTTAATATGTAAATTATAGTTATACCTTGAAATTTCAATTCAAATGCAGACTAA  
 TTATAGGGAATTTGGAAGTGTATCAATAAACAGTATATAATTTT

## **FIGURE 110**

MPPFLLLTCLFITGTSVSPVALDPCSAYISLNEPWRNTDHQLDESQGPFLCDNHVNGEWYHFTGMAGDAMP  
TFCIPENHCGTHAPVWLNGSHPLEGDGIVQRQACASFNGNCCLWNTTVEVKACPGGYVYRLTKPSVCFHV  
YCGHFYDIDCEDCHGSCSDTSECTCAPGTVLGPDRQTCFENECEQNNGGCSEICVNLKNSYRCECGVGRV  
LRSDGKTCEDVEGCHNNNGGCSHSLGSEKGYQCECPRLVLSEDNHTCQVPVLCKSNAIEVNIPRELVGG  
LELFLTNTSCRGVSNNGTHVNILFSLKTCGTVDVVDKIVASNLVTGLPKQTPGSSGDFIIRTSKLLIPVT  
CEFPRLYTISEGYVPNLRNSPLEIMSRNHGIFPFTLEIFKDNEFEPEPYREALPTLKLKRDLSLYFGIEPVVHV  
SGLESLVESCFATPTS KIDEVLKYILIRDGCVSDDSVKQYTSRDHLAKHFQVPVFKFVGKDHKEVFLHCRV  
LVCGVLDERSRCAQCCHRRMRRRCAGGEDSAGLQCQTTLTGGPRIIDWED

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-16

#### **N-glycosylation sites.**

amino acids 89-93, 116-120, 259-263, 291-295, 299-303

#### **Tyrosine kinase phosphorylation sites.**

amino acids 411-418, 443-451

#### **N-myristoylation sites.**

amino acids 226-232, 233-239, 240-246, 252-258, 296-302, 300-306,  
522-528, 531-537

#### **Aspartic acid and asparagine hydroxylation site.**

amino acids 197-209

#### **ZP domain proteins.**

amino acids 431-457

#### **Calcium-binding EGF-like proteins.**

amino acids 191-212, 232-253

## FIGURE 111

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCCTGCACTCGG  
GCCTCCTCCAGCCAGTGTCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGACCTGTGTGGGGAGGCCCT  
CCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAGACCGGGAGGATCACAGAGCCAGCATGT  
TACAGGATCCTGACAGTGATCAACCTCTGAACAGCCTCGATGTCAAACCCCTGCGCAAACCCCGTATCCCC  
ATGGAGACCTTCAGAAAGGTGGGATCCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGT  
GGTTGTCTCATCAAGGTGATTCTGGATAAATACTACTTCTCTGCGGGCAGCCTCTCCACTTCATCCCGA  
GGAAGCAGCTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTC  
CCCGAAGGGCCTGCAGTGGCAGTCCGCCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGGACTCGGCCAC  
AGGGAATGGTTCTCTGCCTGTTTCGACAACCTTCACAGAAGCTCTCGCTGAGACAGCCTGTAGGCAGATGG  
GCTACAGCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGATGTTGTTGAAATCACAGAAAAACGCCAG  
GAGCTTCGCATGCGGAACCTCAAGTGGGCCCTGTCTCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCCTG  
TGGGAAGAGCCTGAAGACCCCCCGTGTGGTGGGTGGGGAGGAGCCTCTGTGGATTCTTGGCCTTGGCAGG  
TCAGCATCCAGTACGACAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCTCACGGCA  
GCCCCACTGCTTCAGGAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAACTGGGCAG  
CTTCCCATCCCTGGCTGTGGCCAAAGATCATCATCATTGAATTCAACCCCATGTACCCCAAGACATGACA  
TCGCCCTCATGAAGCTGCAGTTCCCACTCACTTTCTCAGGCACAGTCAGGCCCATCTGTCTGCCCTTCTTT  
GATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGATGGGGCTTTACGAAGCAGAATGGAGGGAA  
GATGTCTGACATACTGCTGCAGGCGTCAGTCCAGGTCATTGACAGCACACGGTGCAATGCAGACGATGCGT  
ACCAGGGGGAAGTCACCGAGAAGATGATGTGTGCAGGCATCCCGGAAGGGGTGTGGACACCTGCCAGGGT  
GACAGTGGTGGGCCCTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGG  
CTGCGGGGGCCCCGAGCACCCCAAGGATATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATGTCT  
GGAAGGCTGAGCTGTAATGTCTGCTGCCCCCTTTCAGTGTCTGGGAGCCGCTTCCTTCCTGCCCTGCCACCT  
GGGGATCCCCCAAAGTCAGACACAGAGCAAGAGTCCCCCTGGGTACACCCCTCTGCCACAGCCTCAGCAT  
TTCTTGGAGCAGCAAAGGGCCTCAATTCTGTAAAGAGCCCTCGCAGCCAGAGGCGCCAGAGGAAGTCA  
GCAGCCCTAGCTCGGCCCACTTGGTGTCTCCAGCATCCCAGGGAGAGACACAGCCCACTGAACAAGGTCT  
CAGGGGTATTGCTAAGCCAAGAAGGAACCTTCCACACTACTGAATGGAAGCAGGCTGTCTTGTAAAAGCC  
CAGATCACTGTGGGCTGGAGAGGAGAAGGAAAGGGTCTGCGCCAGCCCTGTCCGTCTTACCCATCCCCAA  
GCCTACTAGAGCAAGAAACAGTTGTAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTTACCT  
ACTGTTGTCAATTGTTATTACAGCTATGGCCACTATTATTAAAGAGCTGTGTAACATCTCTGGCAAAAAAA  
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## **FIGURE 112**

MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPITIIALLSLASIIIVVVLIKVILDKYYFLCG  
QPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDN  
FTEALAEACRQMGYSRAVEIGPDQDLVDVEITENSQELMRNSSGPCLSGSLVSLHCLACGKSL  
KTPRVVGGEASVDSWPWQVSIQYDKQHVCSSILDPHWLTAHCFRKHTDVFNWKVRAGSDKL  
GSFPSLAVAKIIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATPLWIIIGWG  
FTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTQCQGDSSGGLMYQS  
DQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEI

**Transmembrane domain:**

amino acids 32-53 (typeII)

## FIGURE 113

GGCTGGACTGGAACCTCCTGGTCCCAAGTGATCCACCCGCTCAGCCTCCCAAGGTGCTGTGATTA  
TAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACTTTTTCAGCAACTAAAAAGCCACAGGAGT  
TGAAGTGTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCCTACTCCTACCTACATTAAAATC  
TGTTTTTTGTCTCTTGTAAGTACCTTTACCTTCCTAACACAGAGGATCTGTCACTGTGGCTCT  
GGCCCAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCACACCGTCCCCCTCGAAG  
CCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTCACCAACTGTCTCACGTCT  
GGAGGCACTGACTCGGGCAGTGACGCTAGCTGAGCCTCTTGGTAGCTGCGGCTTTCAAGGTGGGC  
CTTGCCCTGGCCGTAGAAGGGATTGACAAGCCCGAAGATTTTCATAGGCGATGGCTCCCACTGCCC  
AGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGGCCAGGACGGGCGTGACACCTGTCTCA  
GAAGCAGTGGGTGAGACATCACGCTGCCCCGCCATCTAACCTTTTCATGTCCTGCACATCACCTG  
ATCCATGGGCTAATCTGAACTCTGTCCCAAGGAACCCAGAGCTTGAGTGAGCTGTGGCTCAGACC  
CAGAAGGGGTCTGCTTAGACCACCTGGTTTATGTGACAGGACTTGCAATTCTCCTGGAACATGAGG  
GAACGCCGGAGGAAAGCAAAGTGGCAGGGAAGGAACCTGTGCCAAATTATGGGTGAGAAAAGATG  
GAGGTGTTGGGTTATCACAAGGCATCGAGTCTCCTGCATTCAAGTGACATGTGGGGGAAGGGCTG  
CCGATGGCGCATGACACACTCGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCCGAT  
CCACGTACCAGCTGCTGAAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAA  
TCTGCGATCACCAGCCAGGGGAGCCGCTCTGGGAAGGAGCAAGCAAAGTGACCATTCTCCTCCC  
CTCCTTCCCTCTGAGAGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGG  
GGCTAATGGCTCAGTGTTGGCCAGGAGGTGAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCT  
GTGCGAACACGGAAATGCCTCCAGTAAGCACAGGCTGCAAAATCCCCAGGCAAAGGACTGTGTGG  
CTCAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCAAGACCAAGGAGCTAGAGCTTGTTT  
CAAATGATCTCCAAGGGCCCTTATACCCAGGAGACTTTGATTTGAATTTGAAACCCCAAATCCA  
AACCTAAGAACCAGGTGCATTAAGAATCAGTTATTGCGGGGTGTGGTGGCCTGTAATGCCAACAT  
TTTGGGAGGCCGAGGCGGGTAGATCACCTGAGGTGAGGAGTTCAAGACCAGCCTGGCCAACATGG  
TGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGTGTGTGCCTGTATC  
CCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGTGAAGGAGGCTGAGACA  
GGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGAAAAATAAAAAAGAATTA  
TGGTTATTTGTAA

## **FIGURE 114**

MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLPKPDLHSGTRTEVSTHTVPSKPGTASPC  
WPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFGGGPCPGRRRD

**Signal peptide:**  
amino acids 1-15

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## FIGURE 115

CAGCAGTGGTCTCTCAGTCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCATGGCAA  
AGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCCAAGAAA  
ATATGTAAATCACTTAAGATTTGTGGACTGGTGTGGTATCCTGGCCCTAACTCTAATTGTCCT  
GTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACATGGAGCACACTT  
TCTACAGCAATGGAGAGAAGAAGAAGATTACATGGAAATTGATCCTGTGACCAGAAGTGAATA  
TTCAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTTTAAAAACGGATACACTGG  
CATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAACTCAGATTAAAGTGATTTCCTGAATTTT  
CTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACCACAACTTTCTTTGAACAGTCAGTG  
ATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGATTTTCTTAAAAATTCCAAAATTCTGGA  
GATTTGTGATAACGTGACCATGTATTGGATCAATCCCACTCTAATATCAGTTTCTGAGTTACAAG  
ACTTTGAGGAGGAGGGAGAAGATCTTCACTTTCTGCCAACGAAAAAAGGGATTGAACAAAAT  
GAACAGTGGGTGGTCCCTCAAGTGAAAGTAGAGAAGACCCGTCACGCCAGACAAGCAAGTGAGGA  
AGAAGTCCAATAAATGACTATACTGAAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAG  
GTTATTGTTGTATTTACTGCCGTCGAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTA  
GGCTACTACCCATATCCATACTGCTACCAAGGAGGACGAGTCATCTGTCGTGTCATCATGCCTTG  
TAACTGGTGGGTGGCCCGCATGCTGGGGAGGGTCTTAATAGGAGGTTTGAGCTCAAATGCTTAAAC  
TGCTGGCAACATATAATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCT  
GGTAGCCAGCTCTCCAGAATTACTTGTAGGTAATTCCTCTCTTCATGTTCTAATAAACTTCTACA  
TTATCACCAAAAAAAAAAAAAAAAAA

## **FIGURE 116**

MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPPKKAYDME  
HTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLVHDFKNGYTGIIYFVGLQKCFIKTQIKVIP  
EFSEPEEEIDENEEITTTFFEQSVIWWPAEKPIENRDFLKNSKILEICDNVTMYWINPTLISVSE  
LQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDYTENGIEFDPMLD  
ERGYCCIIYCRGNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWVARMLGRV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-40

**Transmembrane domain:**

amino acids 25-47 (type II)

**N-glycosylation sites.**

amino acids 94-97, 180-183

**Glycosaminoglycan attachment sites.**

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-  
242

**N-myristoylation sites.**

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

**Microbodies C-terminal targeting signal.**

amino acids 315-317

**Cytochrome c family heme-binding site signature.**

amino acids 9-14



## FIGURE 117

GAGCTCCCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCGCAGGCGGCA  
 GGGCGGGCGGCCAGGATCATGTCCACCACCACATGCCAAGTGGTGGCGTTCCCTCCTGTCCATCCTGGGGCT  
 GGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCAGGACCTGTACGACAACCCCGTCACCT  
 CCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGCGTGAGGCAGAGTTCCAGGCTTCACCGAATGCAGGCCC  
 TATTTACACCATCCTGGGACTTCCAGCCATGCTGCAGGCAGTGCAGGCCCTGATGATCGTAGGCATCGTCTCT  
 GGGTGCCATTGGCCTCCTGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTG  
 CCAAAGCCAACATGACACTGACCTCCGGGATCATGTTTCATTGTCTCAGGTCTTTGTGCAATTGCTGGAGTG  
 TCTGTGTTTGCCAAACATGCTGGTGACTAACTTCTGGATGTCCACAGCTAACATGTACACCGGCATGGGTGG  
 GATGGTGCAGACTGTTCCAGACCAGGTACACATTTGGTGGCGCTCTGTTCTGGTGGGCTGGGTGGGAGGCC  
 TCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGGCCTGGCACCAGAAGAAACCAACTACAAA  
 GCGGTTTCTTATCATGCCTCAGGCCACAGTGTTCCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTT  
 TGGGTCCAACACCAAAAACAAGATATACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTTATC  
 CTTCCAAGCACGACTATGTGTAATGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCA  
 CCCAAAAACAAGGAGATCCCATCTAGATTTCTTCTTGCTTTTGACTCACAGCTGGAAGTTAGAAAAGCCT  
 CGATTTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCCACCATAAAACA  
 GCTGAGTTATTTATGAATTAGAGGCTATAGCTCAGATTTTCAATCCTCTATTCTTTTAAATATAACT  
 TTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCTCACATTTTGATGATTTAGACAGACTCCCCCTC  
 TTCTCCTAGTCAATAAACCCATTGATGATCTATTTCCAGCTTATCCCCAAGAAAACCTTTTGAAGGAAA  
 GAGTAGACCCAAAGATGTTATTTTCTGCTGTTTGAATTTGTCTCCCCACCCCAACTTGAGTAGTAATAA  
 ACACTTACTGAAGAAGAAGCAATAAGAGAAAGATATTTGTAATCTCTCCAGCCCATGATCTCGGTTTCTT  
 ACACTGTGATCTTAAAAGTTACCAAACCAAGTCATTTTCAGTTTGAGGCAACCAACCTTTCTACTGCTG  
 TTGACATCTTCTTATTACAGCAACACCATTCTAGGAGTTTCCCTGAGCTCTCCACTGGAGTCCTCTTCTGT  
 CGCGGGTCAGAAATGTCCCTAGATGAATGAGAAAATTATTTTTTTAATTTAAGTCCTAAATATAGTTAA  
 AATAAATAATGTTTGTAGTAAATGATACACTATCTCTGTGAAATAGCCTCACCCTACATGTGGATAGAAG  
 GAAATGAAAAAATAATTGCTTTGACATTGTCTATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATTC  
 ATGAAAAGCTCACACCTGTAATCCTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCCAGAAGT  
 TCGAGACTAGCCTGGGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAATCAGCCAGTCA  
 TGGTGGCATACACCTGTAGTCCCAGCATTCGGGAGGCTGAGGTGGGAGGATCACTTGAGCCCAGGAGGT  
 TGGGGCTGCAGTGAGCCATGATCACACCACTGCACTCCAGCCAGGTGACATAGCGAGATCCTGTCTAAAAA  
 AATAAAAAATAAATAATGAACACAGCAAGTCTTAGGAAGTAGGTAAAACTAATCTTTAA

## **FIGURE 118**

MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLRSCVRQSSGFTECRP  
YFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIMFIVSGL  
CAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTLIGGVMMCIA  
CRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTEDEVQSYPSKH  
DY  
V

### **Signal peptide:**

amino acids 1-23

### **Transmembrane domains:**

amino acids 81-100, 121-141, 173-194

## FIGURE 119

GGAAAACTGTTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCCGGAGTCC  
AGCTGGCTAAAACATCCCAGAGGATAAATGGCAACCCATGCCTTAGAAATCGCTGGGCTGTTTCTTG  
GTGGTGTGGAATGGTGGGCACAGTGGCTGTCACTGTGCCTCAGTGGAGAGTGTGGCCTTCATT  
GAAAACAACATCGTGGTTTTTGAACCTTCTGGGAAGGACTGTGGATGAATTGCGTGAGGCAGGCTAA  
CATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGGCTCTTCTCCGGACCTACAGGCAGCCAGAG  
GACTGATGTGTGCTGCTTCCGTGATGTCTTCTGGCTTTCATGATGGCCATCCTTGGCATGAAATGC  
ACCAGGTGCACGGGGGACAATGAGAAGGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCAT  
CATCACGGGCATGGTGGTGCTCATCCCTGTGAGCTGGGTTGCCAATGCCATCATCAGAGATTTCTATA  
ACTCAATAGTGAATGTTGCCAAAAACGTGAGCTTGAGAAGCTCTCTACTTAGGATGGACCAGGCA  
CTGGTGCTGATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTGTGTGCAACGAAAAGAGCAGTAGCTA  
CAGATACTCGATACCTTCCATCGCACAAACCAAAAAAGTTATCACACCGGAAAGAAGTCACCGAGCG  
TCTACTCCAGAAGTCAGTATGTAGTTGTGTATGTTTTTTAACTTTACTATAAAGCCATGCAAATG  
ACAAAAATCTATATTACTTTTCAAAATGGACCCCAAGAAACTTTGATTTACTGTTCTTAACTGCCT  
AATCTTAATTACAGGAAGTGTGCATCAGCTATTTATGATTCTATAAGCTATTTACAGAGAATGAGATA  
TTAAACCCCAATGCTTTGATTGTTCTAGAAAGTATAGTAATTTGTTTTCTAAGGTGGTTCAAGCATCTA  
CTCTTTTTATCATTACTTCAAAATGACATTGCTAAAGACTGCATTATTTACTACTGTAATTTCTCC  
ACGACATAGCATTATGTACATAGATGAGTGAACATTTATATCTCACATAGAGACATGCTTATATGGT  
TTTATTTAAATGAAATGCCAGTCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAA  
ATCATGGATAGGGTTGAAGAAGGTACTATTAATTGTTTAAAAACAGCTTAGGGATTAATGTCCTCCA  
TTTATAATGAAGATTAAATGAAGGCTTTAATCAGCATTGTAAAGGAAATTGAATGGCTTTCTGATAT  
GCTGTTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTTATCCTCTTCTCCAGAGGCTTTTTTTTT  
CTTGTGTATTAAATTAACATTTTTTAAACGCAGATATTTGTCAAGGGGCTTTGCATTCAAACCTGCTT  
TTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATGGTTTTAGGAAAGTG  
AAAAATTTTTTGTGTTTTGTTTTGAAGAAGATGATGCATTTTGACAAGAAATCATATATGTATGGAT  
ATATTTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATCAATATAAATAAAGAGCAGAAAAATA  
TGTCTTGGTTTTTCATTTGCTTACCAAAAAACAACAACAAAAAAGTTGTCCTTTGAGAACTTCACCT  
GCTCCTATGTGGGTACCTGAGTCAAATTTGTCATTTTGTCTGTGAAAAATAAATTCCTTCTTGTA  
CCATTTCTGTTTAGTTTTACTAAATCTGTAAATACIGTATTTTCTGTTTATTCCAAATTTGATGAA  
ACTGACAATCCAATTTGAAAGTTTGTGTCGACGTCTGTCTAGCTTAAATGAATGTGTTCTATTGCTT  
TATACATTTATATTAATAAATTGTACATTTTCTAATT

## **FIGURE 120**

MATHALEIAGLFLGGVGMVGTVAVTVMPPQWRVSAFIENNIVVFENFWGLWMNCVRQANIRMQCK  
IYDSLLALSPDLQAARGLMCAASVMSFLAFMAILGMKCTRCTGDNEKVKAHILLTAGIIFIITG  
MVLIPVSWVANAIIRDYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVFCCNEKSSSY  
RYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

### **Signal peptide:**

amino acids 1-17

### **Transmembrane domains:**

amino acids 82-101, 118-145, 164-188

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## **FIGURE 121**

GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCGGAG  
CCAGACGCTGACCACGTTCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCCGCGAGCC  
GGGAGCCATGCGACCCCAGGGCCCCGCGCCTCCCCGAGCGGCTCCGCGGCCTCCTGCTGCTCC  
TGCTGCTGCAGCTGCCCCGCGCGTTCGAGCGCCTCTGAGATCCCCAAGGGGAAGCAAAAGGCGCAG  
CTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAGCAGGAGTGCC  
TGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTGGGATCCCAGGTGCGGATG  
GATTCAAAGGAGAAAAGGGGAATGTCTGAGGGAAGCTTTGAGGAGTCCTGGACACCCAACCTAC  
AAGCAGTGTTTCATGGAGTTCATTGAATTATGGCATAGATCTTGGGAAAATTGCGGAGTGACATT  
TACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCA  
GAAATGCATGCTGTCAGCGTTGGTATTTACATTCAATGGAGCTGAATGTTTCAGGACCTCTTCCC  
ATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCACAATTAATATTCATCG  
CACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG  
TTGGCACTTGTTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATC  
ATTATTGAAGAACTACCAAAATTAAATGCTTTAATTTTCATTTGCTACCTCTTTTTTTATTATGCC  
TTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAG  
CTAAATATGTTTACAGACCAAAGTGATTTACACTGTTTTTAAATCTAGCATTATTCATTTTG  
CTTCAATCAAAGTGTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATT  
CTCTCAACCTATAATTTGGAATATTGTTGTTGCTTTTTGTTTTTCTCTTAGTATAGCATTTTTTA  
AAAAATATAAAAGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGT  
TAAATAAAAATTATTTCCAACA

## **FIGURE 122**

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGGKQKAQLRQREVVDLYNGMCLQGPAQVPGR  
DGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAECTFTK  
MRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYLDQGSPEMNSTINIHRTS  
SVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIEELPK

### **Signal peptide:**

amino acids 1-30

### **Transmembrane domain:**

amino acids 195-217

## FIGURE 123

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCTGAA  
CTGGGTGCTCATCAGGGAAGTCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAGCCCCAA  
ATTGCTTGAAGAATACATCATGTTTTTCGATAAGAAGAAATTGTAGGATCCAGTTTTTTTTTTA  
ACCGCCCCCTCCCCACCCCAAAAACTGTAAAGATGCAAAAACGTAATATCCATGAAGATCC  
TATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTGGGATTTATTTGTTCTTGGAG  
TGTTCTGCGTGGCTGGCAAGAATAATGTTCCAAAATCGGTCCATCTCCAAGGGGTCCAATTTT  
TCTTCTGGGTGTGAGCGAGCCCTGACTCACTACAGTGCAGCTGACAGGGGCTGTCATGCAACTG  
GCCCCAAGCCAAAGCAAAAGACCTAAGGACGACCTTTGAACAATACAAAGGATGGGTTTCAATG  
TAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTTATAGCCCCACTGTCTTACTGACAATG  
CTTTCTTCTGCCGAACGAGGATGCCCTAAGGGCTGTAGGTGTGAAGGCAAAATGGTATATTGTGA  
ATCTCAGAAATTACAGGAGATACCCTCAAGTATATCTGCTGGTTGCTTAGGTTTGTCCCTTCGCT  
ATAACAGCCTTCAAAAACCTAAGTATAATCAATTTAAAGGGCTCAACCAGCTCACCTGGCTATAC  
CTTGACCATAACCATATCAGCAATATTGACGAAAATGCTTTTAAATGGAATACGCAGACTCAAAGA  
GCTGATTCTTTAGTTCCAATAGAATCTCCTATTTTCTTAACAATACCTTCAGACCTGTGACAAAT  
TACGGAACCTGGATCTGTCTATAATCAGCTGCATTCTCTGGGATCTGAACAGTTTCGGGGCTTG  
CGGAAGCTGCTGAGTTTACATTTACGGTCTAACTCCCTGAGAACCATCCCTGTGCGAATATTCCA  
AGACTGCCGCAACCTGGAACCTTTTGGACCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATG  
TCTTTGCTGGCATGATCAGACTCAAAGAACTTCACCTGGAGCACAATCAATTTTCCAAGCTCAAC  
CTGGCCCTTTTCCAAGGTTGGTCAGCCTTCAGAACCTTTACTTGCAGTGAATAAAATCAGTGT  
CATAGGACAGACCATGTCTGGACCTGGAGCTCCTTACAAAGGCTTGATTATCAGGCAATGAGA  
TCGAAGCTTTTCACTGGACCCAGTGTTTTCCAGTGTGTCCCGAATCTGCAGCGCCTCAACCTGGAT  
TCCAACAAGCTCACATTTATTGGTCAAGAGATTTTGGATTCTTGGATATCCCTCAATGACATCAG  
TCTTGCTGGGAATATATGGGAATGCAGCAGAAATATTTGCTCCCTTGTAAGCTGGCTGAAAAGTT  
TTAAAGGTCTAAGGGAGAATACAATATCTGTGCCAGTCCCAAAGAGCTGCAAGGAGTAAATGTG  
ATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAAGTACTACAGAGAGGTTTGATCTGGCCAG  
GGCTCTCCCAAAGCCGACGTTTAAAGCCCAAGCTCCCCAGGCCGAAGCATGAGAGCAAACCCCTT  
TGCCCCCGACGGTGGGAGCCACAGAGCCCGCCAGAGACCGATGCTGACGCCGAGCACATCTCT  
TTCCATAAAATCATCGCGGGCAGCGTGGCGCTTTTCTGTCCGTGCTCGTCATCCTGCTGGTTAT  
CTACGTGTCTATGGAAGCGGTACCCTGCGAGCATGAAGCAGCTGCAGCAGCGCTCCCTCATGCGAA  
GGCAGAGGAAAAAGAAAGACAGTCCCTAAAGCAAATGACTCCCAGCACCCAGGAATTTATGTA  
GATTATAAACCACCAACACGGAGACCGAGATGCTGCTGAATGGGACGGGACCCCTGCACCTA  
TAACAAATCGGGCTCCAGGGAGTGTGAGGTATGCAACCATTGTGATAAAAAGAGCTCTTAAAGCT  
GGGAATAAGTGTGCTTTTATTGAACCTCTGGTGACTATCAAGGGAACGCGATGCCCCCTCCCC  
TTCCCTCTCCCTCTCACTTTGGTGGCAAGATCCTTCTTGTCCGTTTTAGTGCATTATAAATACT  
GGTCATTTTCTCTCATACATAATCAACCCATTGAAATTTAAATACCACAATCAATGTGAAGCTT  
GAACTCCGGTTTTAATATAATACCTATTGTATAAGACCCCTTACTGATTCCATTAAATGTGCATTT  
GTTTTAAGATAAACTTCTTTTCATAGGTAAAAA

## **FIGURE 124**

MGFNVIRLLSGSAVALVIAPTIVLLTMLSSAERGCPKGCRCGKMVYCESQKLQEIPSSISAGCLG  
LSLRYNLSLQKLKYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELILSSNRISYFLNNTFR  
PVTNLRNLDLSYNQLHSLGSEQFRGLRKLSSLHLRSNSLRITPVRIQDCRNLELLDLGYNRIRS  
LARNVFAGMIRLKEHLEHNQFSKLNALFPRLVSLQNLQWNKISVIGQTMSWTWSSLQRLDL  
SGNEIEAFSGPSVVFQCVPNLQRLNLDNKLTFIQEILDSWISLNDISLAGNIWECSRNICSLVN  
WLKSFKGLRENTIICASPKELOGVNVIDAVKNYSICGKSTTERFDLARALPKPTFKPKLPRPKHE  
SKPPLPPTVGATEPGPETDADAHEHISFHKIIAGSVALFLSVLVILLVIYVSWKRYPASMKQLQQR  
SLMRRHRKKKRQSLKQMTPTSTQEFYVDYKPTNTETSEMLLNGTGPCCTYNKSGSRECEV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 420-442

**N-glycosylation sites.**

amino acids 126-129, 357-360, 496-499, 504-507

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 465-468

**Tyrosine kinase phosphorylation site.**

amino acids 136-142

**N-myristoylation sites.**

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512



## FIGURE 125

CCGTTATCGTCTTGCGCTACTGCTGAATGTCCGTCCCGAGGAGGAGGAGAGGCTTTTGCCGCTG  
ACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGGCCGAGCT  
AGCAACCTTTCCCTGGATCTCACAAAACCTCGACTCCAAATGCAAGGAGAAGCAGCTCTTGCTC  
GGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACAGCCCTAGGGATC  
ATTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCATTTACAGACACGTAGT  
GTATTCTGGAGGTCGAATGGTCACATATGAACATCTCCGAGAGGTTGTGTTTGGCAAAAGTGAAG  
ATGAGCATTATCCCCTTTGAAATCAGTCATTGGAGGGATGATGGCTGGTGTATTGGCCAGTTT  
TTAGCCAATCCAACCTGACCTAGTGAAGGTTGAGATGCAAATGGAAGGAAAAGGAACTGGAAGG  
AAAACCATGCGATTTCTGTTGTACATCATGCATTTGCAAAAATCTTAGCTGAAGGAGGAATAC  
GAGGGCTTTGGGCAGGCTGGGTACCCAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTA  
ACCACTTATGATACAGTGAAACACTACTTGGTATTGAATACACCACTTGAGGACAATATCATGAC  
TCACGGTTTTATCAAGTTTATGTTCTGGACTGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCA  
TCAAAAGCAGAATAATGAATCAACCACGAGATAAACAAGGAAGGGGACTTTTGTATAAATCATCG  
ACTGACTGCTTGATTGAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTTACC  
ATCTTGGCTGAGAATGACCCCTTGGTCAATGGTGTCTGGCTTACTTATGAAAAATCAGAGAGA  
TGAGTGGAGTCAGTCCATTTTAA

## **FIGURE 126**

MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMGEAALARLGDGARES  
APYRGMVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGGRMVTYEHLEVVFGKSEDEHYPLWKS  
VIGGMMAGVIGQFLANPTDLVKVQMOMEGRKLEGKPLRFRGVHHAFAKILAEGGIRGLWAGWVP  
NIQRAALVNMGDLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCGLVASILGTPADVIKSRIMNQF  
RDKQGRGLLYKSSTDCLIQAVQGEFMSLYKGFLPSWLRMTPWSMVFWLTYEKIREMSGVSPF

### **Transmembrane domains:**

amino acids 25-38, 130-147, 233-248

## FIGURE 127

CGCGGATCGGACCCAAGCAGGTCGGCGGGCGGCGGAGAGCGGCCGGCGTCAGCTCCTCGAC  
CCCCGTGTCGGGCTAGTCCAGCGAGGCGGACGGGCGGCGTGGGCCCATGGCCAGGCCCGGCATGG  
AGCGGTGGCGCGACCGGCTGGCGCTGGTGACGGGGGCTCGGGGGGCATCGGCGCCGCGTGGCC  
CGGGCCCTGGTCCAGCAGGGACTGAAGGTGGTGGGCTGCGCCCGCACTGTGGGCAACATCGAGGA  
GCTGGCTGCTGAATGTAAGAGTGCAGGCTACCCCGGGACTTTGATCCCTACAGATGTGACCTAT  
CAAATGAAGAGGACATCCTCTCCATGTTCTCAGCTATCCGTTCTCAGCACAGCGGTGTAGACATC  
TGCATCAACAATGCTGGCTTGGCCCGGCTGACACCCTGCTCTCAGGCAGCACCAGTGGTTGGAA  
GGACATGTTCAATGTGAACGTGCTGGCCCTCAGCATCTGCACACGGGAAGCCTACCAGTCCATGA  
AGGAGCGGAATGTGGACGATGGGCACATCATTAACATCAATAGCATGTCTGGCCACCGAGTGTTA  
CCCCGTGCTGTGACCCACTTCTATAGTGCCACCAAGTATGCCGTCACTGCGCTGACAGAGGGACT  
GAGGCAAGAGCTTCGGGAGGCCCAGACCCACATCCGAGCCACGTGCATCTCTCAGGTGTGGTGG  
AGACACAATTGCGCTTCAAACCTCCAGCACAAGGACCCTGAGAAGGCAGCTGCCACCTATGAGCAA  
ATGAAGTGTCTCAAACCCGAGGATGTGGCCGAGGCTGTTATCTACGTCTCAGCACCCCGCACA  
CATCCAGATTGGAGACATCCAGATGAGGCCACGGAGCAGGTGACCTAGTGACTGTGGGAGCTCC  
TCCTTCCCTCCCCACCCTTCATGGCTTGCCTCCTGCCTCTGGATTTTAGGTGTTGATTCTGGAT  
CACGGGATACCACTTCTGTCCACACCCCGACCAGGGGCTAGAAAATTTGTTTGAGATTTTATA  
TCATCTTGTCAAATTGCTTCAGTTGTAAATGTGAAAAATGGGCTGGGGAAAGGAGGTGGTGTCCC  
TAATTGTTTTACTTGTTAACTTGTCTTGTGCCCCCTGGGCACTTGGCCTTTGTCTGCTCTCAGTG  
TCTTCCCTTTGACATGGGAAAGGAGTTGTGGCCAAATCCCCATCTTCTGCACCTCAACGTCTG  
TGGCTCAGGGCTGGGGTGGCAGAGGGAGGCCTTCACCTTATATCTGTGTTGTTATCCAGGGCTCC  
AGACTTCCTCCTCTGCCTGCCCCACTGCACCCTCTCCCCCTATCTATCTCCTTCTCGGCTCCCC  
AGCCCAGTCTTGGCTTCTTGTCCCTCCTGGGGTCATCCCTCCACTCTGACTCTGACTATGGCAG  
CAGAACACCAGGGCCTGGCCCAGTGGATTTCATGGTGATCATTAAGAAAGAAAATCGCAACCAA  
AAAAAAAAA

## **FIGURE 128**

MARPGMERWRDRLALVTGASGGIGAARALVQQGLKVVCARTVGNIEELAAECKSAGYPGTLI  
PYRCDLSNEEDILSMFSAIRSQHSQVDICINNAGLARPDTLISGSTSGWKDMFNVNVLALSICTR  
EAYQSMKERNVDDGHIININMSGHRVLPVSVTHFYATKYAVTALTEGLRQELREAQTHIRATC  
ISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVLSTPAHIQIGDIQMRPTEQVT

**Important features of the protein:**

**Signal peptide:**

amino acids 1-17

**N-myristoylation sites.**

amino acids 18-24, 21-27, 22-28, 24-30, 40-46, 90-96, 109-115,  
199-205

**Short-chain alcohol dehydrogenase.**

amino acids 30-42, 104-114

## FIGURE 129

AACTTCTACATGGGCCTCCTGCTGCTGGTGTCTTCCCTCAGCCTCCTGCCGGTGGCCTACACCAT  
CATGTCCCTCCCACCCTCCTTTGACTGCGGGCCGTTTCAGGTGCAGAGTCTCAGTTGCCCCGGGAGC  
ACCTCCCCCTCCCGAGGCAGTCTGCTCAGAGGGCCTCGGCCCAAGATTCCAGTTCTGGTTTCATGC  
CAGCCTGTAAAAGGCCATGGAACCTTTGGGTGAATCACCGATGCCATTAAAGAGGGTTTTCTGCCA  
GGATGGAAATGTTAGGTCGTTCTGTGTCTGCGCTGTTTCATTTAGTAGCCACCAGCCACCTGTGG  
CCGTTGAGTGCTTGAAATTGAGGAAGTGAAGAAATTAATTTCTCATGTATTTTCTCATTTATTTA  
TTAATTTTTAACTGATAGTTGTACATATTTGGGGGTACATGTGATATTTGGATACATGTATACAA  
TATATAATGATCAAATCAGGGTAAGTGGGATATCCATCACATCAAACATTTATTTTTTATTCTTT  
TTAGACAGAGTCTCACTCTGTACCCAGGCTGGAGTGCAGTGGTGCCATCTCAGCTTACTGCAAC  
CTCTGCCTGCCAGGTTCAAGCGATTCTCATGCCTCCACCTCCCAAGTAGCTGGGACTACAGGCAT  
GCACCACAATGCCCAACTAATTTTTGTATTTTAGTAGAGACGGGGTTTTGCCATGTTGCCCAGG  
CTGGCCTTGAACCTCCTGGCCTCAAACAATCCACTTGCCTCGGCCTCCCAAAGTGTTATGATTACA  
GGCGTGAGCCACCGTGCCTGGCCTAAACATTTATCTTTTCTTTGTGTTGGGAAGTTTGAAATTAT  
ACAATGAATTATTGTTAACTGTCATCTCCCTGCTGTGCTATGGAACACTGGGACTTCTTCCCTCT  
ATCTAACTGTATATTTGTACCAGTTAACCAACCGTACTTCATCCCCACTCCTCTCTATCCTTCCC  
AACCTCTGATCACCTCATTCTACTCTCTACCTCCATGAGATCCACTTTTTTAGCTCCCACATGTG  
AGTAAGAAAATGCAATATTTGTCTTTCTGTGCCTGGCTTATTTCACTTAACATAATGACTTCCTG  
TTCCATCCATGTTGCTGCAATGACAGGATTTTCGTTCTTAATTTCAATTAAATAACACACATG  
GCAAAAA

## **FIGURE 130**

MGLLLLVLFLSLLPVAYTIMSLPPSFDCGPFRCRVSVAREHLPSRGSLLRGPRPRIPVLVSCQPV  
KGGHTLGESPMPPFKRVFCQDGNVRSFCVCAVHFSSHQPPVAVECLK

Important features of the protein:

Signal peptide:

amino acids 1-18

N-myristoylation site.

amino acids 86-92

Zinc carboxypeptidases, zinc-binding region 2 signature.

amino acids 68-79

## FIGURE 131

TTCTGAAGTAACGGAAGCTACCTTGTATAAAGACCTCAACACTGCTGACCATGATCAGCGCAGCCTGGAGC  
ATCTTCCTCATCGGGACTAAAATTGGGCTGTTCCCTTCAAGTAGCACCTCTATCAGTTATGGCTAAATCCTG  
TCCATCTGTGTGCTCGCTGCGATGCGGGTTTCATTTACTGTAATGATCGCTTTCTGACATCCATTCCAACAG  
GAATACCAGAGGATGCTACAACCTCTACCTTCAGAACAACCAATAAATAATGCTGGGATTCCCTTCAGAT  
TTGAAAACTTGCTGAAAGTAGAAGAATATACCTATAACCACAACAGTTTAGATGAATTCCTACCAACCT  
CCCAAAGTATGTAAGAGTTACATTTGCAAGAAAATAACATAAGGACTATCACTTATGATTCACTTTCAA  
AAATTCCTATCTGGAAGAATTACATTTAGATGACAACCTGTCTCTGCAGTTAGCATAGAAGAGGAGCA  
TTCCGAGACAGCAACTATCTCCGACTGCTTTTCCCTGTCCCGTAATCACCTTAGCACAATTCCTGGGGTTT  
GCCCAGGACTATAGAAGAACTACGCTTGGATGATAATCGCATATCCACTATTTATCACCATCTCTTCAAG  
GTCTCACTAGTCTAAAACGCTGGTTCTAGATGGAACCTGTTGAACAATCATGGTTTAGGTGACAAAGTT  
TTCTTCAACCTAGTTAATTTGACAGAGCTGTCCCTGGTGGGAATTCCTGACTGCTGCACCAGTAACCT  
TCCAGGCACAAACCTGAGGAAGCTTTATCTTCAAGATAACCACATCAATCGGGTGGCCCCAATGCTTTTT  
CTTATCTAAGGCAGCTCTATCGACTGGATATGTCCAATAATAACCTAAGTAATTTACCTCAGGGTATCTTT  
GATGATTTGGACAATATAACACAACCTGATTCTTCGCAACAATCCCTGGTATTGCGGGTGCAAGATGAAATG  
GGTACGTGACTGGTTACAATCACTACCTGTGAAGGTCAACGTGCGTGGGCTCATGTGCCAAGCCCCAGAAA  
AGGTTCTGGGGATGGCTATTAAAGGATCTCAATGCAGAACTGTTTGATTGTAAGGACAGTGGGATTGTAAGC  
ACCATTAGATAACCAGTCAATACCCAACAGTGTATCTGCCCAAGGACAGTGGCCAGCTCCAGTGAC  
CAACAGCCAGATATTAAGAACCCCAAGCTCACTAAGGATCAACAAACCACAGGGAGTCCCTCAAGAAAAA  
CAATTACAATTACTGTGAAGTCTGTACCTCTGATACCATTCAATCTCTTGGAACTTGCTCTACCTATG  
ACTGCTTTGAGACTCAGCTGGCTTAACTGGGCCATAGCCCGCATTTGGATCTATAACAGAAACAATTGT  
AACAGGGGAACGCAGTGAGTACTTGGTCACAGCCCTGGAGCCTGATTACCCCTATAAAGTATGCATGGTTC  
CCATGGAACACAGCAACCTCTACCTATTTGATGAACTCCTGTTTGTATTGAGACTGAAACTGCACCCCTT  
CGAATGTACAACCTACAACCACCCTCAATCGAGAGCAAGAGAAAGAACCTTACAAAAACCCCAATTTACC  
TTTGGCTGCCATCATTGGTGGGGCTGTGGCCCTGGTTACCATTGCCCTTCTTGCTTTAGTGTGTGGTATG  
TTCATAGGAATGGATCGCTCTTCTCAAGGAACCTGTGCATATAGCAAAGGGAGGAGAAGAAAGGATGACTAT  
GCAGAAGCTGGCACTAAGAAGGACAACCTATCCTGGAAATCAGGGAAACTTCTTTTCAGATGTTACCAAT  
AAGCAATGAACCATCTCGAAGGAGGAGTTTGTAAATACACCATATTTCTCCTAATGGAATGAATCTGT  
ACAAAAACAATCACAGTGAAAGCAGTAGTAACCGAAGCTACAGAGACAGTGGTATTCAGACTCAGATCAC  
TCACACTCATGATGCTGAAGGACTCACAGCAGACTTGTGTTTTGGGTTTTTTTAAACCTAAGGAGGTGATG  
GT

## **FIGURE 132**

MISAAWSIFLIGTKIGLFLQVAPLSVMAKSCPSVCRCDAGFIYCNDRFLTSIPTGIPEDATTLYL  
QNNQINNAGIPSDLKNLLKVERIYLYHNSLDEFPTNLPKYVKELHLQENNIRTITYDSLSKIPYL  
EELHLDDNSVSAVSIEEGAFRDSNYLRLLFLSRNHLSTIPWGLPRTIEELRLDDNRISTISSPSL  
QGLTSLKRLVLDGNLLNNHGLGDKVFFNLVNLTELSLVRNSLTAAPVNLPGTNLRKLYLQDNHIN  
RVPPNAFSYLRQLYRLDMSNNNLSNLPQIGIFDDLNDITQLILRNNPWYCGCKMKWVRDWLQSLPV  
KVNVRGLMCQAPEKVRGMAIKDLNAELFDCKDSGIVSTIQITTAIPNTVYPAQQQWPAPVTKQPD  
IKNPKLTKDQQTGSPSRKTTITITVKSVTSDTIHISWKLALPMTALRLSWLKLGHSPAFGSITET  
IVTGERSEYLVTALEPDSPYKVCMPMETSNLYLFDETPVCJETETAPLRMYNPPTTLNREQEKE  
PYKNPNPLAAIIGGAVALVTIALALVCWYVHRNGSLFSRNCAYSKGRRRKDDYAEAGTKKDNS  
ILEIRETSFQMLPISNEPISKEEFVIHTIFPPNGMNLKNNHSESSSNRSYRDSGIPDSDHSHS

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-28

#### **Transmembrane domain:**

amino acids 531-552

#### **N-glycosylation sites.**

amino acids 226-229, 282-285, 296-299, 555-558, 626-629, 633-636

#### **Tyrosine kinase phosphorylation site.**

amino acids 515-522

#### **N-myristoylation sites.**

amino acids 12-17, 172-177, 208-213, 359-364, 534-539, 556-561,  
640-645

#### **Amidation site.**

amino acids 567-570

#### **Leucine zipper pattern.**

amino acids 159-180

#### **Phospholipase A2 aspartic acid active site.**

amino acids 34-44



## FIGURE 133

CCGTCATCCCCCTGCAGCCACCCTTCCCAGAGTCCTTTGCCAGGCCACCCAGGCTTCTTGCCA  
GCCCTGCCGGGCCACTTGTCTTCAATGTCTGCCAGGGGGAGGTGGGAAGGAGGTGGGAGGAGGGCG  
TGCAGAGGCAGTCTGGGCTTGGCCAGAGCTCAGGGTGCTGAGCGTGTGACCAGCAGTGAGCAGAG  
GCCGGCCATGGCCAGCCTGGGGCTGCTGCTCCTGCTCTTACTGACAGCACTGCCACCGCTGTGGT  
CCTCCTCACTGCTGGGCTGGACACTGCTGAAAGTAAAGCCACCATTGCAGACCTGATCCTGTCT  
GCGCTGGAGAGAGCCACCGTCTTCCTAGAACAGAGGCTGCCTGAAATCAACCTGGATGGCATGGT  
GGGGGTCCGAGTGCTGGAAGAGCAGCTAAAAAGTGTCGGGAGAAGTGGGCCAGGAGCCCTGC  
TGCAGCCGCTGAGCCTGCGCGTGGGGATGCTGGGGGAGAAGCTGGAGGCTGCCATCCAGAGATCC  
CTCCACTACCTCAAGCTGAGTGATCCCAAGTACCTAAGAGAGTTCCAGCTGACCCTCCAGCCCGG  
GTTTTGGAAGCTCCCACATGCTGGATCCACACTGATGCCCTCCTTGGTGTACCCACGTTCCGGG  
CCCAGGACTCATTCTCAGAGGAGAGAAGTGACGTGTGCCTGGTGCAGCTGCTGGGAACCGGGACG  
GACAGCAGCGAGCCCTGCGGCCTCTCAGACCTCTGCAGGAGCCTCATGACCAAGCCCGGCTGCTC  
AGGCTACTGCCTGTCCCACCAACTGCTCTTCTTCTCTGGGCCAGAATGAGGGGATGCACACAGG  
GACCACTCCAACAGAGCCAGGACTATATCAACCTCTTCTGCGCCAACATGATGGACTTGAACCGC  
AGAGCTGAGGCCATCGGATACGCCCTACCCTACCCGGGACATCTTCATGGAACATCATGTTCTG  
TGGAATGGGCGGCTTCTCCGACTTCTACAAGCTCCGGTGGCTGGAGGCCATTCTCAGCTGGCAGA  
AACAGCAGGAAGGATGCTTCGGGGAGCCTGATGCTGAAGATGAAGAATTATCTAAAGCTATTCAA  
TATCAGCAGCATTTTTTCGAGGAGAGTGAAGAGGCGAGAAAAACAATTTCCAGATTCTCGCTCTGT  
TGCTCAGGCTGGAGTACAGTGGCGCAATCTCGGCTCACTGCAACCTTTGCCTCCTGGGTTCAGC  
AATTCTCTTGCTCATCCTCCCGAGTAGCTGGGACTACAGGAGCGTGCCACCATACTGGCTAAT  
TTTTATATTTTTTTAGTAGAGACAGGGTTTCATCATGTTGCTCATGCTGGTCTCGAACTCCTGAT  
CTCAAGAGATCCGCCACCTCAGGCTCCCAAAGTGTTGGGATTATAGGTGTGAGCCACCGTGTCTG  
GCTGAAAAGCACTTTCAAAGAGACTGTGTTGAATAAAGGGCCAAGGTTCTTGCCACCCAGCACTC  
ATGGGGGCTCTCTCCCCTAGATGGCTGCTCCTCCACAACACAGCCACAGCAGTGGCAGCCCTGG  
GTGGCTTCCTATACATCCTGGCAGAATACCCCCAGCAAACAGAGAGCCACACCCATCCACACCG  
CCACCACCAAGCAGCCGCTGAGACGGACGGTTCCATGCCAGCTGCCTGGAGGAGGAACAGACCCC  
TTTAGTCCTCATCCCTTAGATCCTGGAGGGCACGGATCACATCCTGGGAAGAAGGCATCTGGAGG  
ATAAGCAAAGCCACCCGACACCCAATCTTGAAGCCCTGAGTAGGCAGGGCCAGGGTAGGTGGG  
GGCCGGGAGGGACCCAGGTGTGAACGGATGAATAAAGTTCAACTGCAACTGAAAAAAAAA

## **FIGURE 134**

MSARGRWEGGRRACRGSIGLARAQGAERTVSSEQRPMASLGLLLLLLLTALPPLWSSSLPGLD  
TAESKATIADLILSALERATVFLEQRLPEINLDGMVGVRVLEEQLKSVREKWAQEPLLQPLSLRV  
GMLGEKLEAAIQRSYLKLSDPKYLREFQLTLQPGFWKLPHAWIHTDASLVYPTFGPQDSFSEE  
RSDVCLVQLLGTGTDSSPCGLSDLCRSLMTKPGCSGYCLSHQLLFFLWARMRGCTQGPLQSQD  
YINLFCANMDLNRRAEAIGYAYPTRDIEMENIMFCMGGFSDFYKLRWLEAILSWQKQEGCFG  
EPDAEDEELSKAIQYQQHFSRRVKRREKQFPDSRSVAQAGVQWRNLGSLQPLPPGFKQFSLILP  
SSWDYRSVPPYLANFYIFLVETGFHHVAHAGLELLISRDPTSGSQSVGL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 39-56

**Tyrosine kinase phosphorylation sites.**

amino acids 149-156, 274-282

**N-myristoylation sites.**

amino acids 10-16, 20-26, 63-69, 208-214

**Amidation site.**

amino acids 10-14

**Glycoprotein hormones beta chain signature 1.**

amino acids 230-237

## FIGURE 135

GGTCTGAGTGCAGAGCTGCTGTCATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCTGCTGCTG  
CTGCTGCTATCGGGGGATGTCCAGAGCTCGGAGGTGCCCCGGGGCTGCTGCTGAGGGATCGGGAGG  
GAGTGGGGTCGGCATAGGAGATCGCTTCAAGATTGAGGGGCGTGAGTTGTTCCAGGGGTGAAGC  
CTCAGGACTGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAG  
ACAGATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCTCC  
AGCTTACAGATTTGATCCCCTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCAAGATATG  
TGAATTACATCAAAACATCAGAGGTTGTGAGACTGCCCTATCCTCTCCAAATGAAATCTTCAGGT  
CCACCTTCTTACTTTATTAAAGGGAATCGTGGGGCTGGACAGACTTTCTAATGAACCCAATGGT  
TATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCTAAAGTGGTCAACACAAGTGATC  
CTGACATGAGACGGGAAATGGAGCAGTCAATGAATATGCTGAATTCCAACCATGAGTTGCCTGAT  
GTTTCTGAGTTCATGACAAGACTCTTCTCTTCAAATCATCTGGCAAATCTAGCAGCGGCAGCAG  
TAAACAGGCAAAAGTGGGGCTGGCAAAGGAGGTAGTCAGGCCGTCCAGAGCTGGCATTGTCAC  
AAACACGGCAACACTGGGTGGCATCCAAGTCTTGAAAACCGTGTGAAGCAACTACTATAAACTT  
GAGTCATCCCGACGTTGATCTCTTACAACGTGTATGTT  
AACTTTTTAGCACATGTTTTGTACTTGGTACACGAGAAAACCCAGCTTTCATCTTTTGTCTGTAT  
GAGGTCAATATTGATGTCACCTGAATTAATTACAGTGTCTATAGAAAATGCCATTAATAAATTAT  
ATGAACTACTATACATTATGTATATTAATTAACATCTTAATCCAGAAATCAAAAAAAAAAAAA  
AAAAAAAAAAAAAA

## **FIGURE 136**

MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPDWISAA  
RVLVDGEEHVGLKTDGSAFVVDIPSGSYVVEVVSAPYRFDVPRVDITSKGKMRARYVNYIKTSE  
VVRLPYPLOMKSSGPPSYFIKRESWGWTDFLMNPMVMMMLVPLLI FVLLPKVVNTSDPDMRREME  
QSMNMLNSNHELDPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGKRR

### **Important features of the protein:**

#### **Signal sequence:**

amino acids 1-23

#### **Transmembrane domain:**

amino acids 161-182

#### **N-glycosylation site.**

amino acids 184-187

#### **Glycosaminoglycan attachment sites.**

amino acids 37-40, 236-239

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 151-154

#### **N-myristoylation sites.**

amino acids 33-38, 36-41, 38-44, 229-234

#### **Amidation site.**

amino acids 238-241

#### **ATP/GTP-binding site motif A (P-loop).**

amino acids 229-236

## FIGURE 137

GATGGCGCAGCCACAGCTTCTGTGAGATTGATTTCTCCCCAGTTCCCTGTGGGTCTGAGGGGA  
CCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATCCCCAAACAA  
GTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCTGTTCCAGGC  
CTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGCCACGACCTGTGC  
CACCAACTCGCACTCAGACTCTGAACCTCAGACCTGAAATCTTCTCTTACGGGAGGCTTGGCAGT  
TTTTCTTACTCCTGTGGTCTCCAGATTTGAGGCTTAAGATGAAAGCCTCTAGTCTTGCCTTCAGC  
CTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAGACACTCAATTTGGG  
AAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGAGATACGGGGCAGTG  
TGCAAGCCAAAGATGGAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAAGACACA  
AAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTCTATCTGGACAGGGTATTTAA  
AAACTACCAGACCCCTGACCATTATATCTCTCCGGAAGATCAGCAGCCTCGCCAATTCCTTTCTTA  
CCATCAAGAAGGACCTCCGGCTCTCTCATGCCACATGACATGCCATTGTGGGGAGGAAGCAATG  
AAGAAATACAGCCAGATTCTGAGTCACCTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGC  
TTTGGGGGAAC TAGACATTTCTTCTGCAATGGATGGAGGAGACAGAATAGGAGGAAAGTGATGCTG  
CTGCTAAGAATATTCGAGGTCAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCAA  
ACCACCATCTCTTTACTGTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTTATGCATTACTTG  
CTTCCTTGATGATTGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGTATAAGATTTT  
TGTAATATCTTTCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTGTCTATTTA  
ATGTATTTATTTTACTTGGACATGAACTTTAAAAAATTCACAGATTATATTTATAACCTG  
ACTAGAGCAGGTGATGTATTTTATACAGTAAAAAATAACCTTGTAATCTAGAAGAGTGG  
CTAGGGGGGTTATTCATTTGTATTCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGAT  
ATTTGAAATTGAACCAATGACTACTTAGGATGGGTTGTGGAATAAGTTTGTGTGGAATTGCAC  
ATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTATCTCCAG  
CCAGGAATCTACACGGCCAGCATGTATTTCTACAAATAAAGTTTCTTTGCATACCAAAAAA  
AAAAA

## **FIGURE 138**

MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTCWALTAEPGWGQNGATTTCATNSHSDSELRPEIF  
SSREAWQFFLLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNG  
FSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFNKYQTPDHYTLRKIS  
SLANSFLTIKDLRLSHAMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEET  
E

Important features of the protein:

Signal peptide:

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141



## **FIGURE 140**

MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHAEPPEPSAGASSNWTTLPPPLF  
SKVVIVLIDALRDDFVFGSKGVKFMPTTYLVEKGASHSFVAEAKPPTVTMPRIKALMTGSLPGF  
VDVIRNLNSPALLEDSDVIRQAKAAGKRIVFYGDETWVKLFPHFVEYDGTTSFFVSDYTEVDNNV  
TRHLDKVLKRGDWDILILHYLGLDGHIGHISGPN SPLIGQKLSEMDSVLMKIHTSLQSKERETPLP  
NLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKPGDIRHPKHVQ

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-34

#### **Transmembrane domain:**

amino acids 58-76

#### **N-glycosylation sites.**

amino acids 56-60, 194-198

#### **N-myristoylation sites.**

amino acids 6-12, 52-58, 100-106, 125-131, 233-239, 270-276,  
275-281, 278-284

#### **Amidation site.**

amino acids 154-158

#### **Cell attachment sequence.**

amino acids 205-208



## **FIGURE 141**

GGCACGAGGCAAGCCTTCCAGGTTATCGTGACGCACCTTGAAAGTCTGAGAGCTACTGCCCTACA  
GAAAGTTACTAGTGCCCTAAAGCTGGCGCTGGCACTGATGTTACTGCTGCTGTTGGAGTACAAC  
TCCCTATAGAAAACAACGCCAGCACCTTAAGACCACTCACACCTTCAGAGTGAAGAACTTAAAC  
CCGAAGAAATTCAGCATTTCATGACCAGGATCACAAAGTACTGGTCCTGGACTCTGGGAATCTCAT  
AGCAGTTCAGATAAAAACACATACGCCAGAGATCTTCTTTGCATTAGCCTCATCCTTGAGCT  
CAGCCTCTGCGGAGAAAGGAAGTCCGATTCTCTGGGGGTCTCTAAAGGGGAGTTTTGTCTCTAC  
TGTGACAAGGATAAAGGACAAAGTCATCCATCCCTTCAGCTGAAGAAGGAGAACTGATGAAGCT  
GGCTGCCCCAAAAGGAATCAGCACGCCGGCCCTTCATCTTTATAGGGCTCAGGTGGGCTCCTGGA  
ACATGCTGGAGTCGGCGGCTCACCCCGGATGGTTCATCTGCACCTCCTGCAATTGTAATGAGCCT  
GTTGGGGTGACAGATAAATTTGAGAACAGGAAACACATTGAATTTTCATTTCAACCAAGTTTGCAA  
AGCTGAAATGAGCCCCAGTGAGGTCAGCGATTAGGAAACTGCCCCATTGAACGCCCTTCCTCGCTA  
ATTTGAACTAATTGTATAAAAACACCAAACCTGCTCACT

## **FIGURE 142**

MLLLLLLEYNFPIENNCQHLKTTHTFRVKNLNPKKFSIHDQDHKVLVLD SGNLI AVDPDKNYIRPEI  
FFALASSLSSASAEKGSPI LLGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFI  
FYRAQVGSWNMLESAAHPGWFICTSCNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 33-36

**N-myristoylation site.**

amino acids 50-55, 87-92

**Interleukin-1**

amino acids 37-182

## FIGURE 143

CTAGAGAGTATAGGGCAGAAGGATGGCAGATGAGTGACTCCACATCCAGAGCTGCCTCCCTTTAA  
TCCAGGATCCTGTCCTTCCTGTCCTGTAGGAGTGCCTGTTGCCAGTGTGGGGTGAGACAAGTTTG  
TCCCACAGGGCTGTCTGAGCAGATAAGATTAAGGGCTGGGTCTGTGCTCAATTAACCTGTGGG  
CACGGGGGCTGGGAAGAGCAAAGTCAGCGGTGCCTACAGTCAGCACCATGCTGGGCCTGCCGTGG  
AAGGGAGGTCTGTCTGGGCGCTGCTGCTGCTTCTCTTAGGCTCCCAGATCCTGCTGATCTATGC  
CTGGCATTTCACGAGCAAAGGGACTGTGATGAACACAATGTCATGGCTCGTTACCTCCCTGCCA  
CAGTGGAGTTTGCTGTCCACACATTCAACCAACAGAGCAAGGACTACTATGCCTACAGACTGGGG  
CACATCTTGAATTCTGGAAGGAGCAGGTGGAGTCCAAGACTGTATTCTCAATGGAGCTACTGCT  
GGGGAGAACTAGGTGTGGGAAATTTGAAGACGACATTGACAACCTGCCATTTCCAAGAAAGCACAG  
AGCTGAACAATACTTTACCTGCTTCTTCACCATCAGCACCAGGCCCTGGATGACTCAGTTCAGC  
CTCCTGAACAAGACCTGCTTGGAGGGATTCCACTTGAGTGAAACCCACTCACAGGCTTGTCATGT  
GCTGCTCCACATTCCGTGGACATCAGCACTACTCTCCTGAGGACTCTTCAGTGGCTGAGCAGCT  
TTGGACTTGTTTGTATCCTATTTTGCATGTGTTTGAGATCTCAGATCAGTGTTTTAGAAAATCC  
ACACATCTTGAGCCTAATCATGTAGTGTAGATCATTAAACATCAGCATTTTAAGAAAAAAAAAA  
AA

## **FIGURE 144**

MLGLPWKGGLSWALLLLLLLGSQILLIYAWHFHEQRDCDEHNVMARYLPATVEFAVHTFNQQSKDY  
YAYRLGHILNSWKEQVESKTVFSMELLGRTRCGKFEDDIDNCHFQESTELNNTFTCFITSTRP  
WMTQFSLLNKTCLGEGFH

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**N-glycosylation sites.**

amino acids 117-121, 139-143

**N-myristoylation site.**

amino acids 9-15

## FIGURE 145

CTGTGCAGCTCGAGGCTCCAGAGGCACACTCCAGAGAGAGCCAAGGTTCTGACGCGATGAGGAAG  
CACCTGAGCTGGTGGTGGCTGGCCACTGTCTGCATGCTGCTCTTCAGCCACCTCTCTGCGGTCCA  
GACGAGGGGCATCAAGCACAGAATCAAGTGAACCGGAAGGCCCTGCCAGCACTGCCAGATCA  
CTGAGGCCCAGGTGGCTGAGAACCGCCCGGGAGCCTTCATCAAGCAAGGCCGCAAGCTCGACATT  
GACTTCGGAGCCGAGGGCAACAGGTACTACGAGGCCAACTACTGGCAGTTCCCCGATGGCATCCA  
CTACAACGGCTGCTCTGAGGCTAATGTGACCAAGGAGGCATTTGTACCGGCTGCATCAATGCCA  
CCCAGGCGGCGAACCAGGGGAGTTCCAGAAGCCAGACAACAAGCTCCACCAGCAGGTGCTCTGG  
CGGCTGGTCCAGGAGCTCTGCTCCCTCAAGCATTGCGAGTTTTGGTTGGAGAGGGGCGCAGGACT  
TCGGGTCACCATGCACCAGCCAGTGCTCCTCTGCCTTCTGGCTTTGATCTGGCTCATGGTGAAAT  
AAGCTTGCCAGGAGGCTGGCAGTACAGAGCGCAGCAGCGAGCAAATCCTGGCAAGTGACCCAGCT  
CTTCTCCCCCAAACCCACGCGTGTTCTGAAGGTGCCAGGAGCGGCGATGCACTCGCACTGCAAA  
TGCCGCTCCCACGTATGCGCCCTGGTATGTGCCTGCGTTCTGATAGATGGGGGACTGTGGCTTCT  
CCGTCACTCCATTCTCAGCCCCTAGCAGAGCGTCTGGCACACTAGATTAGTAGTAAATGCTTGAT  
GAGAAGAACACATCAGGCACCTGCGCCACCTGCTTCACAGTACTTCCCAACAACCTCTTAGAGGTAG  
GTGTATTCCCGTTTTACAGATAAGGAACTGAGGCCCGAGAGCTGAAGTACTGCACCCAGCATC  
ACCAGCTAGAAAGTGGCAGAGCCAGGATTCAACCCCTGGCTTGTCTAACCCAGGTTTTCTGCTCT  
GTCCAATTCCAGAGCTGTCTGGTGATCACTTTATGTCTCACAGGGACCCACATCCAAACATGTAT  
CTCTAATGAAATTGTGAAAGCTCCATGTTTAGAAATAAATGAAAACACCTGA

## **FIGURE 146**

MRKHLSSWWLATVCMLLFSHLSAVQTRGIKHRIKWNRKALPSTAQITEAQVAENRPGAFIKQGRK  
LDIDFGAEGNRYYEANYWQFPDGIHYNGCSEANVTKEAFVTGTCINATQAANQGEFQKPDNKLHQQ  
VLWRLVQELCSLKHCEFWLERGAGLRVTMHQPVLLCLLALIWLMLVK

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-26

#### **Transmembrane domain:**

amino acids 157-171

#### **N-glycosylation sites.**

amino acids 98-102, 110-114

#### **Tyrosine kinase phosphorylation site.**

amino acids 76-83

#### **N-myristoylation sites.**

amino acids 71-77, 88-94, 93-99, 107-113, 154-160

#### **Amidation site.**

amino acids 62-66

## **FIGURE 147**

GCCTTGGCCTCCCAAAGGGCTGGGATTATAGGCGTGACCACCATGTCTGGTCCAGAGTCTCATT  
CCTGATGATTTATAGACTCAAAGAAAACTATGTTTCAGAAGCTCTCTCTCTTCTGGCCTCCTCT  
CTGTCTTCTTTCCCTCTTTCTTCTTATTTTAATTAGTAGCATCTACTCAGAGTCATGCAAGCTGG  
AAATCTTTCATTTTGCTTGTCAGTGGGGTAGGTCAGTCTTAGTTTTTATTTTTTGAATTT  
CAACTTTCAGATTCAGGGGGTACATGTGAAGGTTTGTTTTATGAGTATATTGCATGATGCTGAGG  
TTTGGGGT

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## **FIGURE 148**

MFRSSLLFWPPLCLLSLFLLLILISSIYSESKLEIFHFACQWGRSLSLSFYFLKFQLSDSGGTCE  
GLFYEYIA

Important features of the protein:

Signal peptide:

amino acids 1-25

N-myristoylation site.

amino acids 62-68

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## FIGURE 149

GTCTCCGCGTCACAGGAACCTTCAGCACCCACAGGGCGGACAGCGCTCCCCCTCTACCTGGAGACTTGAC  
TCCCGCGCGCCCCAACCCCTGCTTATCCCTTGACCGTCGAGTGTGAGAGATCCTGCAGCCGCCAGTCC  
CGGCCCCCTCTCCGCCCCACACCCACCCCTCCTGGCTCTTCTGTTTTTACTCCTCCTTTTCATTGATA  
ACAAAAGCTACAGCTCCAGGAGCCAGCGCGGGCTGTGACCCAAGCCGAGCGTGAAGAATGGGGTT  
CCTCGGGACCGGCACTTGGATTCTGGTGTAGTGCTCCCATTCAAGCTTTCCCCAAACCTGGAGGAA  
GCCAAGACAAATCTCTACATAATAGAGAATTAAGTGCAGAAAGACCTTTGAATGAACAGATTGCTGAA  
GCAGAAGAAGACAAGATTAAAAAACATATCCTCCAGAAAACAAGCCAGGTGAGAGCAACTATTCTTT  
TGTTGATAACTTGAACCTGCTAAAGGCAATAACAGAAAAGGAAAAAATTGAGAAAGAAAGACAATCTA  
TAAGAAGCTCCCCACTTGATAATAAGTTGAATGTGGAAGATGTTGATTCAACCAAGAATCGAAAAGT  
ATCGATGATTATGACTCTACTAAGAGTGGATTGGATCATAAATTTCAAGATGATCCAGATGGTCTTCA  
TCAACTAGACGGGACTCCTTTAACCGCTGAAGACATTGTCCATAAAATCGCTGCCAGGATTTATGAAG  
AAAATGACAGAGCCGTGTTTGACAAGATTGTTCTAACTACTTAATCTCGGCCTTATCACAGAAAGC  
CAAGCACATACACTGGAAGATGAAGTAGCAGAGGTTTACAAAAATTAATCTCAAAGGAAGCCAACAA  
TTATGAGGAGGATCCCAATAAGCCCACAAGCTGGACTGAGAATCAGGCTGGAAAAATACCAGAGAAAG  
TGACTCCAATGGCAGCAATTCAAGATGGTCTTGCTAAGGGAGAAAACGATGAAACAGTATCTAACACA  
TTAACCTTGACAAATGGCTTGGAAGGAGAACTAAACCTACAGTGAAGACAACCTTGAGGAACTCCA  
ATATTTCCCAAATTTCTATGCGCTACTGAAAAGTATTGATTGAGAAAAAGCAAAAGAGAAAGAAA  
CACTGATTACTATCATGAAAACACTGATTGACTTTGTGAAGATGATGGTGAATATGGAACAATATCT  
CCAGAAGAAGGTGTTTCTACCTTGAAAACCTGGATGAAATGATTGCTCTTCAGACCAAAAACAAGCT  
AGAAAAAATGCTACTGACAATATAAGCAAGCTTTTCCAGCACCATCAGAGAAGAGTCATGAAGAAA  
CAGACAGTACCAAGGAAGAAGCAGCTAAGATGGAAGGAATATGGAAGCTTGAAGGATTCACAAAA  
GATGATAACTCCAACCCAGGAGGAAAGACAGATGAACCCAAAGGAAAAACAGAAGCCTATTTGGAAGC  
CATCAGAAAAAATATTGAATGGTTGAAGAAACATGACAAAAAGGGAATAAAGAAGATTATGACCTTT  
CAAAGATGAGAGACTTCATCAATAAACAGCTGATGCTTATGTGGAGAAAGGCATCCTTGACAAGGAA  
GAAGCCGAGGCCATCAAGCGCATTTATAGCAGCTGTAAAAAATGGCAAAAGATCCAGGAGTCTTTCAA  
CTGTTTCAGAAAACATAATATAGCTTAAACACTTCTAATTCTGTGATTAAATTTTTTGACCCAAGG  
GTTATTAGAAAGTGCTGAATTTACAGTAGTTAACCTTTTACAAGTGGTTAAACATAGCTTTCTTCCC  
GTAAAAACTATCTGAAAGTAAAGTTGTATGTAAGCTGAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 150**

MGFLGTGTWILVVLPIQAFPKPGGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPENKPG  
QSNYSFVDNLNLLKAITEKEKIEKERQSIRSSPLDNKLNVEDVDSTKNRKLIDDYDSTKSGLDHK  
FQDDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDEVAE  
VLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTPMAAIQDGLAKGENDETVSNTLTLTNGLE  
RRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKMMVKYGTISPEEGV  
SYLENLDEMIALQTKNLEKNATDNISKLFAPSEKSHEETDSTKEEAAKMEKEYGSLKDSTKDD  
NSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYDLSKMRDFINKQADAYVEKGILDK  
EEAEAIAKRIYSSL

### **N-glycosylation sites:**

amino acids 68-71, 346-349, 350-353

### **Casein kinase II phosphorylation site:**

amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-  
220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-  
341, 369-372, 382-385, 386-389, 387-390

### **N-myristoylation sites:**

amino acids 143-148, 239-244

## FIGURE 151

CGGCTCGAGGCTCCCGCCAGGAGAAAGGAACATTCTGAGGGGAGTCTACACCTGTGGAGCTCAA  
**GATGGT**CCTGAGTGGGGCGCTGTGCTTCCGAATGAAGGACTCGGCATTGAAGGTGCTTTATCTGC  
ATAATAACCAGCTTCTAGCTGGAGGGCTGCATGCAGGGAAGGTCATTAAAGGTGAAGAGATCAGC  
GTGGTCCCCAATCGGTGGCTGGATGCCAGCCTGTCCCCCGTCATCCTGGGTGTCCAGGGTGGAAAG  
CCAGTGCCTGTCTATGTGGGGTGGGGCAGGAGCCGACTCTAACACTAGAGCCAGTGAACATCATGG  
AGCTCTATCTTGGTGCCAAGGAATCCAAGAGCTTCACCTTCTACCGGCGGGACATGGGGCTCACC  
TCCAGCTTCGAGTCCGGCTGCCTACCCGGGCTGGTTCCCTGTGCACGGTGCCTGAAGCCGATCAGCC  
TGTCAGACTCACCCAGCTTCCCGAGAATGGTGGCTGGAATGCCCCATCACAGACTTCTACTTCC  
AGCAGTGTGACT**TAGGGCA**ACGTGCCCCCAGAACTCCCTGGGCAGAGCCAGCTCGGGTGAGGGGT  
GAGTGGAGGAGACCCATGGCGGACAATCACTCTCTCTGCTCTCAGGACCCACAGTGTGACTTAG  
TGGGCACCTGACCACTTTGTCTTCTGGTTCCAGTTTGGATAAATTCTGAGATTTGGAGCTCAGT  
CCACGGTCTCCCCCACTGGATGGTGTCTACTGTGTGGAACTTGTAAAAACCATGTGGGGTAA  
CTGGGAATAACATGAAAAGATTCTGTGGGGGTGGGGTGGGGAGTGGTGGGAATCAITTCCTTAA  
TAATGGTAACGTACAAGTGTTACCCCTGAGCCCGCAGGCCAACCCATCCCCAGTTGAGCCCTTATA  
GGGTCACTAGCTCTCCACATGAAGTCTGTCACTCACCCTGTGCAGGAGAGGGAGGTGGTCATA  
GAGTCAGGGATCTATGGCCCTTGGCCAGCCCCACCCCTTCCCTTTAATCCTGCCACTGTCTATA  
TGCTACCTTTCCCTATCTCTCCCTCATCATCTTGTGTGGGCATGAGGAGGTGGTGTGTGAGAA  
GAAATGGCTCGAGCTCAGAAGATAAAAGATAAGTAGGGTATGCTGATCCTCTTTTAAAAACCCAA  
GATACAATCAAAATCCCAGATGCTGGTCTCTATTCCCATGAAAAGTGCTCATGACATATTGAGA  
AGACCTACTTTACAAAGTGGCATATATTGCAATTTATTTTAAATTAAGATACCTATTATATATT  
TCTTTATAGAAAAAGTCTGGAAGAGTTTACTTCAATTGTAGCAATGTCAGGGTGGTGGCAGTAT  
AGGTGATTTTTCTTTAATTCTGTTAATTTATCTGTATTTCTAATTTTCTACAATGAAGATGA  
ATTCTTGTATAAAAAATAAGAAAAGAAATTAATCTTGAGGTAAGCAGAGCAGACATCATCTCTGA  
TTGTCTCAGCCTCCACTTCCCGAGATAAATTCAAATTGAATCGAGCTCTGCTGCTCTGGTTGG  
TTGTAGTAGTGATCAGGAAACAGATCTCAGCAAAGCCACTGAGGAGGAGGCTGTGCTGAGTTTGT  
GTGGCTGGAATCTCTGGGTAAGGAACCTAAAGAACAAAAATCATCTGGTAATTCTTTCCTAGAAG  
GATCACAGCCCCCTGGGATTCCAAGGCATTGGATCCAGTCTCTAAGAAGGCTGCTGTACTGGTTGA  
ATTGTGTCCCCCTCAAATTCACATCCTTCTTGAATCTCAGTCTGTGAGTTTATTGGAGATAAG  
GTCTCTGCAGATGTAGTTAGTTAAGACAAGGTCATGCTGGATGAAGGTAGACCTAAATCAATAT  
GACTGGTTTCCCTGTATGAAAAGGAGAGGACACAGAGACAGAGGAGACGCGGGGAAGACTATGTA  
AAGATGAAGGCAGAGATCGGAGTTTGCAGCCACAAGCTAAGAAACACCAAGGATTGTGGCAACC  
ATCAGAAGCTTGAAGAGGCAAGAAGAAATCTTCCCTAGAGGCTTTAGAGGGATAACGGCTCTG  
CTGAAACCTTAATCTCAGACTTCCAGCCTCCTGAACGAAGAAAGATAAATTTCCGGCTGTTTTAA  
GCCACCAAGGATAATTGGTTACAGCAGCTCTAGGAAACTAATACAGCTGCTAAATGATCCCTGT  
CTCCTCGTGTTTACATTCTGTGTGTGTCCCTCCACAATGTACCAAGTTGTCTTTGTGACCAA  
TAGAATATGGCAGAAGTGATGGCATGCCACTTCCAAGATTAGGTTATAAAAGACACTGCAGCTTC  
TACTTGAGCCCTCTCTCTGCCCCACCCGCCCAATCTATCTTGGCTCACTCGCTCTGGGGG  
AAGCTAGCTGCCATGCTATGAGCAGGCCTATAAAGAGACTTACGTGGTAAAAAATGAAGTCTCCT  
GCCCACAGCCACATTAGTGAACCTAGAAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTT  
AAGTTGCTCAGTTTTGGTCTAACTTGTATGCAGCAATAGATAAATAATATGCAGAGAAAGAG

## **FIGURE 152**

MVLSGALCFRMKDSALKVLYLHNNQLLAGGLHAGKVIKGEESISVVPNRWLDASLSPVILGVQGGG  
QCLSCGVGQEPTLTLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWFLCTVPEADQP  
VRLTQLPENGGWNAIPITDFYFQQCD

### **N-myristoylation sites.**

amino acids 29-34, 30-35, 60-65, 63-68, 73-78, 91-96, 106-111

### **Interleukin-1 signature.**

amino acids 111-131

### **Interleukin-1 proteins.**

amino acids 8-29, 83-120, 95-134, 64-103

## FIGURE 153

CTTCAGAACAGGTTCTCCTTCCCCAGTCACCCAGTTGCTCGAGTTAGAATTGTCTGCAATGCCCCG  
CCTGCAGAAATCTGTGAGCTCTTTCCTTATGGGGACCCTGGCCACCAGCTGCCTCCTTCTCTTGG  
CCCTCTTGGTACAGGGAGGAGCAGCTGCGCCCATCAGCTCCCACTGCAGGCTTGACAAGTCCAAC  
TTCCAGCAGCCCTATATACCAACCGCACCTTCATGCTGGCTAAGGAGGCTAGCTTGGCTGATAA  
CAACACAGACGTTTCGTCTCATTGGGGAGAACTGTTCCACGGAGTCAGTATGAGTGAGCGCTGCT  
ATCTGATGAAGCAGGTGCTGAACCTTCACCCTTGAAGAAGTGCTGTCCCTCAATCTGATAGGTTT  
CAGCCTTATATGCAGGAGGTGGTGCCCTTCTTGGCCAGGCTCAGCAACAGGCTAAGCACATGTCA  
TATTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAAAGCTGAAGGACACAGTGAAAAAGC  
TTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAAGTGGATTGCTGTTTATGTCTCTGAGAAAT  
GCCTGCATTGACCAGAGCAAAGCTGAAAAATGAATAACTAACCCCTTTCCTGCTAGAAATAA  
CAATTAGATGCCCCAAAGCGATTTTTTTTAAACCAAGGAAGATGGGAAGCCAACTCCATCATG  
ATGGGTGGATTCCAAATGAACCCCTGCGTTAGTTACAAAGGAAACCAATGCCACTTTTGTGTTATA  
AGACCAGAAGGTAGACTTTCTAAGCATAGATATTTATTGATAACATTTTATTGTAAGTGGTGTTT  
TATACACAGAAACAATTTATTTTTTAAATAATTGTCTTTTCCATAAAAAAGATTACTTTCCAT  
TCCTTTAGGGGAAAAAACCCCTAAATAGCTTCATGTTTCCATAATCAGTACTTTATATTTATAAA  
TGTATTTATTATTATTATAAGACTGCATTTTATTTATATCATTTTATTAATATGGATTATTTAT  
AGAAACATCATTCGATATTGCTACTTGAGTGTAAGGCTAATATTGATATTTATGACAATAATTAT  
AGAGCTATAACATGTTTATTTGACCTCAATAAACACTTGGATATCCC

## **FIGURE 154**

MAALQKSVSSFILMGTLATSCLLLLLALLVQGGAAAPISSHCRLDKSNFQQPYITNRTFMLAKEASL  
ADNNTDVRLIGEKLFGVSMSERCYLMKQVLNFTLEEVLPQSDRFQPYMQEVVPFLARLSNRLS  
TCHIEGDDLHIQRNVQKLKDTVKKLGESGEIKAIGELDLLFMSLRNACI

**Important features of the protein:**

**Signal peptide:**

amino acids 1-33

**N-glycosylation sites.**

amino acids 54-58, 68-72, 97-101

**N-myristoylation sites.**

amino acids 14-20, 82-88

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 10-21

## FIGURE 155

GGCTTGCTGAAAATAAAATCAGGACTCCTAACCTGCTCCAGTCAGCCTGCTTCCACGAGGCCTGT  
CAGTCAGTGCCCGACTTGTGACTGAGTGTGCAGTGCCAGCATGTACCAGGTCAGTCAGAGGGC  
TGCCTGAGGGCTGTGCTGAGAGGGAGAGGAGCAGAGATGCTGCTGAGGGTGGAGGGAGGCCAAGC  
TGCCAGGTTTGGGGCTGGGGGCCAAGTGGAGTGAGAACTGGGATCCCAGGGGGAGGGTGCAGAT  
GAGGGAGCGACCCAGATTAGGTGAGGACAGTTCTCTCATTAGCCTTTTCCTACAGGTGGTTGCAT  
TCTTGGCAATGGTCATGGGAACCCACACCTACAGCCACTGGCCCAGCTGCTGCCCCAGCAAAGGG  
CAGGACACCTCTGAGGAGCTGCTGAGGTGGAGCACTGTGCCTGTGCCTCCCCTAGAGCCTGCTAG  
GCCCCAACCGCCACCCAGAGTCTGTAGGGCCAGTGAAGATGGACCCCTCAACAGCAGGGCCATCT  
CCCCCTGGAGATATGAGTTGGACAGAGACTTGAACCGGCTCCCCAGGACCTGTACCACGCCCCGT  
TGCTGTGCCCCGCACTGCGTCAGCCTACAGACAGGCTCCCACATGGACCCCCGGGGCAACTCGGA  
GCTGCTCTACCACAACCAGACTGTCTTCTACAGGCGGCCATGCCATGGCGAGAAGGGCACCCACA  
AGGGCTACTGCCTGGAGCGCAGGCTGTACCGTGTTCCTTAGCTTGTGTGTGTGCGGGCCCCGT  
GTGATGGGCTAGCCGGACCTGCTGGAGGCTGGTCCCTTTTGGGAAACCTGGAGCCAGGTGTACA  
ACCACTTGCCATGAAGGGCCAGGATGCCCAGATGCTTGGCCCCCTGTGAAGTGCTGTCTGGAGCAG  
CAGGATCCCGGGACAGGATGGGGGGCTTTGGGGAAAACCTGCACTTCTGCACATTTTGAAAAGAG  
CAGCTGCTGCTTAGGGCCGCCGGAAGCTGGTGTCTGTCAATTTCTCTCAGGAAAGGTTTTCAAA  
GTTCTGCCCATTCTGGAGGCCACCACTCCTGTCTCTTCTCTTTTCCCATCCCCTGCTACCCTG  
GCCCAGCACAGGCACTTTCTAGATATTTCCCCCTTGCTGGAGAAGAAAGAGCCCCCTGGTTTTATT  
TGTTTGTTTACTCATCACTCAGTGAGCATCTACTTTGGGTGCATTCTAGTGTAGTTACTAGTCTT  
TTGACATGGATGATTCTGAGGAGGAAGCTGTATTGAATGTATAGAGATTTATCCAAATAAATAT  
CTTTATTTAAAAATGAAAAA

## **FIGURE 156**

MRERPRLGEDSSLISLFLQVVAFLAMVMGHTYSHWPSCCPSKGQDTSEELLRWSTVPVPPLEPA  
RPNRHPESCRAEDGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVSLQTGSHMDPRGNS  
ELLYHNQTVFYRRPCHGEKGTHKGYCLERRLYRVSLACVCVRPRVMG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-32

**N-glycosylation site.**

amino acids 136-140

**Tyrosine kinase phosphorylation site.**

amino acids 127-135

**N-myristoylation sites.**

amino acids 44-50, 150-156



## FIGURE 157

CCGGCGATGTCGCTCGTGTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCGGTACCCCGAGAGCC  
GACCGTTCAATGTGGCTCTGAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAATCC  
CCGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAAC TAGTGTGCAACAGGGGACTATTCA  
ATTTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTGTAAGGCCACCAA  
GATTTGTGTGACGGGCAAAGCAACTTCCAGTCTACAGCTGTGTGAGGTGCAATTACACAGAGG  
CCTTCCAGACTCAGACCAGACCCTCTGGTGGTAAATGGACATTTTCCTACATCGGCTTCCTGT  
GAGCTGAACACAGTCTATTTTCATTGGGGCCATAATATTCCTAATGCAAATATGAATGAAGATGG  
CCCTTCCATGTCTGTGAATTTACCTCACCAGGCTGCCTAGACCACATAATGAAATATAAAAAA  
AGTGTGTCAAGGCCGGAAGCCTGTGGGATCCGAACATCACTGCTTGTGAAGAAGATGAGGAGACA  
GTAGAAGTGAAC TTCACAACCACTCCCCTGGGAAACAGATACATGGCTCTTATCCAACACAGCAC  
TATCATCGGGTTTTCTCAGGTGTTTGAGCCACACCAGAAGAAACAAACGCGAGCTTCAGTGGTGA  
TTCCAGTGACTGGGGATAGTGAAGGTGCTACGGTGCAGCTGACTCCATATTTTCCTACTTGTGGC  
AGCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGCCACAAACAGGCGTCCCTTTCCCTCT  
GGATAACAACAAAAGCAAGCCGGGAGGCTGGCTGCCTCTCCTCCTGCTGTCTGTGCTGGTGCCA  
CATGGGTGCTGGTGGCAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTTCCTTT  
TCTACCACCACACTACTGCCCCCATTAAGGTTCTTGTGGTTTACCCATCTGAAATATGTTTCCA  
TCACACAATTTGTTACTTCACTGAATTTCTTCAAACCATTCGAGAAGTGAGGTCATCCTTGAAA  
AGTGGCAGAAAAAGAAAATAGCAGAGATGGGTCCAGTGCAGTGGCTTGCCACTCAAAGAAGGCA  
GCAGACAAAGTCGTCTTCTTCTTCCAATGACGTCAACAGTGTGTGCGATGGTACCTGTGGCAA  
GAGCGAGGGCAGTCCAGTGAGAACTCTCAAGACCTCTTCCCCCTTGCCCTTTAACCTTTCTGCA  
GTGATCTAAGAAGCCAGATTCTCTGCACAAATACGTGGTGGTCTACTTTAGAGAGATTGATACA  
AAAGACGATTACAATGCTCTCAGTGTCTGCCCAAGTACCACCTCATGAAGGATGCCACTGCTTT  
CTGTGCAGAACTTCTCCATGTCAAGCAGCAGGTGTGAGCAGGAAAAAGATCACAAGCCTGCCACG  
ATGGCTGCTGCTCCTTGTAG

## **FIGURE 158**

MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLPGLRDLRVEPVTTSVATGDYSILMNVS  
WRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWTFSYIGFPVELNTVYFIGAHNIP  
NANMNEDGPSMSVNFTSPGCLDHIMKYKKKCVKAGSLWDPNITACKKNEETVEVNFTTTPLGNRYMALIQH  
STIIGFSQVFEPHQKKQTRASVVIPVTGDSEGATVQLTPYFPTCGSDCIRHKGTVVLCPQTGVFPPLDNNK  
SKPGGWLPLLLLSLLVATWVLVAGIYLMWRHERIKKTSFSTTTLLPPIKVLVVYPSEICFHHTICYFTEFL  
QNHCRSEVILEKWQKKKIAEMGPVQWLATQKKAADKVVFLSNDVNSVCDGTCGKSEGSPSENSQDLFPLA  
FNLFCSDLRSQIHLHKYVVVYFREIDTKDDYNALSVC PKYHLMKDATAFCAELLHVKKQVSAGKRSQACHD  
GCCSL

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-14

#### **Transmembrane domain:**

amino acids 290-309

#### **N-glycosylation sites.**

amino acids 67 - 71, 103 - 107, 156 - 160, 183 - 187, 197 - 201 and 283  
- 287

#### **cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 228 - 232 and 319 - 323

#### **Casein kinase II phosphorylation sites.**

amino acids 178 - 182, 402 - 406, 414 - 418 and 453 - 457

#### **N-myristoylation site.**

amino acids 116-122

#### **Amidation site.**

amino acids 488-452

## FIGURE 159

AGCCACCAGCGCAACATGACAGTGAAGACCCTGCATGGCCCAGCCATGGTCAAGTACTTGCTGCT  
GTCGATATTGGGGCTTGCCTTTCTGAGTGAGGCGGCAGCTCGGAAAATCCCCAAAGTAGGACATA  
CTTTTTTCCAAAAGCCTGAGAGTTGCCCCGCTGTGCCAGGAGGTAGTATGAAGCTTGACATTGGC  
ATCATCAATGAAAACCAGCGCGTTTCCATGTCACGTAACATCGAGAGCCGCTCCACCTCCCCCTG  
GAATTACACTGTCACTTGGGACCCCAACCGGTACCCCTCGGAAGTTGTACAGGCCCAGTGTAGGA  
ACTTGGGCTGCATCAATGCTCAAGGAAAGGAAGACATCTCCATGAATCCGTTCCCATCCAGCAA  
GAGACCCTGGTCGTCCGGAGGAAGCACCAAGGCTGCTCTGTTTCTTTCCAGTTGGAGAAGGTGCT  
GGTGACTGTTGGCTGCACCTGCCGTCACCCCTGTCATCCACCATGTGCAGTTAAGAGGTGCATATCC  
ACTCAGCTGAAGAAG

## **FIGURE 160**

MTVKTLHGPMVKYLLLSILGLAFLSEAAARKIPKVGHTFFQKPESCPPVPGGSMKLDIGIINEN  
QRVSMSRNIESRSTSPWNYTWTWDPNRYPSEVVQAQCRNLGCINAQGKEDISMNSVPIQQETLVV  
RRKHQGC SVSFQLEKVLVTVGCTCVTPVIHHVQ

### **Signal sequence:**

amino acids 1-30

### **N-glycosylation site.**

amino acids 83-87

### **N-myristoylation sites.**

amino acids 106-111, 136-141

## FIGURE 161

A C A C T G G C C A A A C A A A A C G A A A G C A C T C C G T G C T G G A A G T A G G A G G A G A G T C A G G A C T C C C A G G  
 A C A G A G A G T G C A C A A A C T A C C C A G C A C A G C C C C C T C C G C C C C C T C T G G A G G C T G A A G A G G G A T T C  
 C A G C C C C T G C C A C C C A C A G A C A C G G G C T G A C T G G G G T G T C T G C C C C C C T T G G G G G G G G C A G C A C  
 A G G G C C T C A G G C C T G G G T G C C A C C T G G C A C C T A G A A G A T G C C T G T G C C C T G G T T C T T G C T G T C C T  
 T G G C A C T G G G C C G A A G C C C A G T G G T C C T T T C T C T G G A G A G G C T T G T G G G G C C T C A G G A C G C T A C C  
 C A C T G C T C T C C G G G C C T C T C C T G C C G C C T C T G G G A C A G T G A C A T A C T C T G C C T G C C T G G G G A C A T  
 C G T G C C T G C T C C G G G C C C C G T G C T G G C G C C T A C G C A C C T G C A G A C A G A G C T G G T G C T G A G G T G C C  
 A G A A G G A G A C C G A C T G T G A C C T C T G T C T G C G T G T G G C T G T C C A C T T G G C C G T G C A T G G G C A C T G G  
 G A A G A G C C T G A A G A T G A G G A A A G T T T G G A G G A G C A G C T G A C T C A G G G G T G G A G G A G C C T A G G A A  
 T G C C T C T C T C C A G G C C A A G T C G T G C T C T C C T T C C A G G C C T A C C C T A C T G C C C G C T G C G T C C T G C  
 T G G A G G T G C A A G T G C C T G C T G C C C T T G T G C A G T T T G G T C A G T C T G T G G G C T C T G T G G T A T A T G A C  
 T G C T T C G A G G C T G C C C T A G G G A G T G A G G T A C G A A T C T G G T C C T A T A C T C A G C C C A G G T A C G A G A A  
 G G A A C T C A A C C A C A C A C A G C A G T G C C T G C C C T G C C C T G C C T C A A C G T G T C A G C A G A T G G T G A C A  
 A C G T G C A T C T G G T T C T G A A T G T C T C T G A G G A G C A G C A C T T C G G C C T C T C C C T G T A C T G G A A T C A G  
 G T C C A G G G C C C C C A A A A C C C G G T G G C A C A A A A C C T G A C T G G A C C G C A G A T C A T T A C C T T G A A  
 C C A C A G A C C T G G T T C C C T G C C T C T G T A T T C A G G T G T G G C C T C T G G A A C C T G A C T C C G T T A G G A  
 C G A A C A T C T G C C C C T T C A G G G A G A C C C C G C G C A C A C C A G A A C C T C T G G C A A G C C G C C G A C T G  
 C G A C T G C T G A C C C T G C A G A G C T G G C T G C T G G A C G C A C C G T G C T C G C T G C C C G C A G A A G C G G C A C T  
 G T G C T G G C G G G C T C C G G G T G G G G A C C C C T G C C A G C C A C T G G T C C C A C C G C T T C C T G G G A G A A C G  
 T C A C T G T G G A C A A G G T T C T C G A G T T C C A T T G C T G A A A G G C C A C C C T A A C C T C T G T G T T C A G G T G  
 A A C A G C T C G G A G A A G C T G C A G C T G C A G G A G T G C T T G T G G G C T G A C T C C C T G G G G C C T C T C A A A G A  
 C G A T G T G C T A C T G T T G G A G A C A C G A G G C C C C A G G A C A A C A G A T C C C T C T G T G C C T T G G A A C C C A  
 G T G G C T G T A C T T C A C T A C C C A G C A A A G C C T C C A C G A G G G C A G C T C G C C T T G G A G A G T A C T T A C T A  
 C A A G A C C T G C A G T C A G G C C A G T G T C T G C A G C T A T G G G A C G A T G A C T T G G G A G C G C T A T G G G C C T G  
 C C C C A T G G A C A A A T A C A T C C A C A A G C G C T G G G C C C T C G T G T G G C T G G C C T G C C T A C T C T T T G C C G  
 C T G C G C T T T C C C T C A T C C T C C T T C T C A A A A A G G A T C A C G C G A A A G G G T G G C T G A G G C T C T T G A A A  
 C A G G A C G T C C G C T C G G G G G C G G C C C A G G G G C C G C G C G G C T C T G C T C C T A C T C A G C C G A T G A  
 C T C G G G T T T C G A G C C C T G G T G G G C G C C C T G G C G T C G G C C C T G T G C C A G C T G C C G C T G C G C G T G G  
 C C G T A G A C C T G T G G A G C C G T C G T G A A C T G A G C G C G C A G G G C C C G T G G C T T G G T T T C A C G C G C A G  
 C G G C G C C A G A C C C T G C A G A G G G C G G C G T G G T G G T C T T G C T C T T C T C C C G G T G C G G T G G C G C T  
 G T G C A G C A G T G G C T A C A G G A T G G G G T G T C C G G G C C G G G G C G C A C G G C C C G C A C G A C G C C T T C C  
 G C G C C T C G C T C A G C T G C G T G C T G C C C G A C T T C T T G C A G G G C C G G G C G C C C G G C A G C T A C G T G G G G  
 G C C T G C T T C G A C A G G C T G C T C C A C C C G A C G C C G T A C C C G C C T T T T C C G A C C G T G C C C G T C T T  
 C A C A C T G C C C T C C C A A C T G C C A G A C T T C C T G G G G G C C C T G C A G C A G C C T C G C G C C C C G C T T C C G  
 G G C G G C T C C A A G A G A G A G C G G A G C A A G T G T C C C G G G C C C T T C A G C C A G C C C T G G A T A G C T A C T T C  
 C A T C C C C C G G G G A C T C C C G C G C C G G G A C G C G G G T G G G A C C A G G G G C G G A C C T G G G C C G G G G A  
 C G G G A C T T A A T A A A G G C A G A C G C T G T T T T T C T A A A A A A

## **FIGURE 162**

MPVPWFLLSLALGRSPVVLRLVGPQDATHCSPGLSCRLWDSIILCLPGDIVPAPGPVLAPTHLQTELV  
LRCQKETDCDLCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNASLQAQVVLSEQAYPTARCVLLEV  
QVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTPRYEKELNHTQQLPALPWLNVNSADGDNVHLVLNV  
EEQHFGLSLYWNQVQGPPKPRWHKNLTGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQ  
LWQAARLRLTLQSWLLDAPCSLPAAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQ  
VNSSEKLQEQECLWADSLGPLKDDVLLLETRGPQDNRSLEPSGCTSLPSKASTRAARLGEYLLQDLQS  
GQCLQLWDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSLILLKKDHAKGWLRLKQDVRSAAAARG  
RAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGFVAWFHAQRRQTLQEGGVVLLFSP  
GAVALCSEWLQDGVSGPGAHGPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRLHHPDAVPALFRTVPVFT  
LPSQLPDFLQALQPPRPRSGRLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT

### **Signal sequence:**

amino acids 1-20

### **Transmembrane domain.**

amino acids 453-475

### **N-glycosylation sites.**

amino acids 118-121, 186-189, 198-201, 211-214, 238-241, 248-251,  
334-337, 357-360, 391-394

### **Glycosaminoglycan attachment site.**

amino acids 583-586

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 552-555

### **N-myristoylation sites.**

amino acids 107-112, 152-157, 319-324, 438-443, 516-521, 612-617,  
692-697, 696-701, 700-705

## FIGURE 163

GGGAGGGCTCTGTGCCAGCCCCGATGAGGACGCTGCTGACCATCTTGACTGTGGGATCCCTGGCT  
 GCTCAGCCCCCTGAGGACCCCTCGGATCTGCTCCAGCACGTGAAATCCAGTCCAGCAACTTTGA  
 AAACATCCTGACGTGGGACAGCGGGCCAGAGGGCACCCAGACACGGTCTACAGCATCGAGTATA  
 AGACGTACGGAGAGAGGGACTGGGTGGCAAAGAAGGGCTGTGAGCGGATCACCCGGAAGTCCTGC  
 AACCTGACGGTGGAGACGGGCAACCTCACGGAGCTCTACTATGCCAGGGTCACCGCT  
 GTCAGTGCGGGAGGCCGGTCAGCCACCAAGATGACTGACAGGTTGAGTCTCTGACGACACTAC  
 CCTCAAGCCACCTGATGTGACCTGTATCTCAAAGTGAGATCGATTGAGATGATTGTTTCATCCTA  
 CCCCCACGCCAATCCGTGCAGGCGATGGCCACCGGCTAACCTGGAAGACATCTTCCATGACCTG  
 TTCTACCACTTAGAGCTCCAGGTCAACCGCACCTACCAAATGCACCTTGGAGGGAAGCAGAGAGA  
 ATATGAGTTCTTCGGCCTGACCCCTGACACAGAGTTCTTGGCACCATCATGATTTGCGTTCCCA  
 CCTGGGCCAAGGAGAGTGCCCCCTACATGTGCCGAGTGAAGACACTGCCAGACCGGACATGGACC  
 TACTCCTTCTCCGGAGCCTTCCTGTTCTCCATGGGCTTCCTCGTCGAGTACTCTGCTACCTGAG  
 CTACAGATATGTACCAAGCCGCTGCACCTCCCAACTCCCTGAACGTCCAGCGAGTCCCTGACTT  
 CTCAGCGCTGCGCTTCATCCAGGAGCAGTCTGATCCCTGTCTTTGACCTCAGCGGCCCCAGC  
 AGTCTGGCCCCAGCCTGTCCAGTACTCCAGATCAGGGTGTCTGGACCCAGGGAGCCCCGAGGAGC  
 TCCACAGCGGCATAGCCTGTCCGAGATCACCTACTTAGGGCAGCCAGACATCTCCATCCTCCAGC  
 CCTCCAACGTGCCACCTCCCCAGATCCTCTCCCCACTGTCTATGCCCCAAACGCTGCCCTGAG  
 GTCGGGCCCCCATCTATGCACCTCAGGTGACCCCCGAAGCTCAATTCCCATTTCTACGCCCCACA  
 GGCCATCTCTAAGGTCCAGCCTTCCTCCTATGCCCCCTCAAGCCACTCCGGACAGCTGGCCTCCCT  
 CCTATGGGGTATGCATGGAAGTTCTGGCAAAGACTCCCCACTGGGACACTTTCTAGTCCTAAA  
 CACCTTAGGCCTAAAGGTGAGCTTCAGAAAGAGCCACCAGCTGGAAGCTGCATGTTAGGTGGCCT  
 TTCTCTGCAGGAGGTGACCTCCTTGGCTATGGAGGAATCCCAAGAAGCAAAATCATTGCACCAGC  
 CCCTGGGGATTTGCACAGACAGAATCTGACCCAAATGTGCTACACAGTGGGGAGGAAGGGACA  
 CCACAGTACCTAAAGGGCCAGCTCCCCCTCCTCCTCAGTCCAGATCGAGGGCCACCCCATGTC  
 CCTCCCTTTGCAACCTCCTTCCGGTCCATGTTCCCCCTCGGACCAAGGTCCAAGTCCCTGGGGCC  
 TGCTGGAGTCCCTTGTGTGTCCCAAGGATGAAGCCAAGAGCCAGCCCCCTGAGACCTCAGACCTG  
 GAGCAGCCCCACAGAAGTGGATTCTTTTTTCAGAGGCCTGGCCCTGACTGTGAGTGGGAGTCCTG  
 AGGGGAATGGGAAAGGCTTGGTGCTTCTCCTGTCCTACCCAGTGTGACATCCTTGGCTGTCA  
 ATCCCATGCCTGCCCATGCCACACACTCTGCGATCTGGCCTCAGACGGGTGCCCTTGAGAGAAGC  
 AGAGGGAGTGGCATGCAGGGCCCCCTGCCATGGGTGCGCTCCTCACCGGAACAAAGCAGCATGATA  
 AGGACTGCAGCGGGGAGCTCTGGGGAGCAGCTGTGTAGACAAGCGCGTGCTCGCTGAGCCCTG  
 CAAGGCAGAAATGACAGTGCAAGGAGGAAATGCAGGGAACCTCCCGAGGTCCAGAGCCCCACCTC  
 CTAACACCATGGATTCAAAGTGCTCAGGGAATTTGCCTCTCCTTGCCCCATTCTTGCCAGTTTC  
 ACAATCTAGCTCGACAGAGCATGAGGCCCTGCCTCTTCTGTGATTGTTCAAAGGTGGGGAAGAGA  
 GCCTGGAAAAGAACCAGGCCTGGAAAAGAACCAGAAGGAGGCTGGGCAGAACCAAGAACCTGC  
 ACTTCTGCCAAGGCCAGGGCCAGCAGGACGGCAGGACTCTAGGGAGGGGTGTGGCCTGCAGCTCA  
 TTCCCAGCCAGGGCAACTGCCTGACGTTGCACGATTTGAGCTTCATTCTCTGATAGAACAAAGC  
 GAAATGCAGGTCCACCAGGGAGGGAGACACACAAGCCTTTTCTGCAGGCAGGAGTTTCAGACCT  
 ATCTGAGAATGGGGTTTGAAGGAAGGTGAGGGCTGTGGCCCTGGACGGGTACAATAACACAC  
 TGTACTGATGTCACAACTTTGCAAGCTCTGCCCTTGGGTTGAGCCCATCTGGGCTCAAATTCAGC  
 CTCACCACTCACAAGCTGTGTGACTTCAAACAAATGAAATCAGTGCCAGAACCTCGGTTTCCTC  
 ATCTGTAATGTGGGGATCATAACACCTACCTCATGGAGTTGTGGTGAAGATGAAATGAAGTCATG  
 TCTTTAAAGTGCTTAATAGTGCCTGGTACATGGGCAGTGCCCAATAACGGTAGCTATTTAAAAA  
 AAAAAAA

## **FIGURE 164**

MRTLLTILTVGSLAAHAPEDPSDLLQHVKFQSSNFENILTWDSGPEGTPDTVYSIEYKTYGERDW  
VAKKGCQRITRKSCNLTVETGNLTLEYARVTAVSAGGRSATKMTDRFSSLQHTTLKPPDVTICIS  
KVRSIQMIVHPTPTPIRAGDGHRLTLEDIFHDLFYHLELQVNRTYQMHGKGKQREYEFFGLTPDT  
EFLGTIMICVPTWAKESAPYMCRVKTLPDRTWTYSFSGAFLFSMGFLVAVLCYLSYRYVTKPPAP  
PNSLNVQRVLTFQPLRFIQEHVLIPVFDLSGPSSLAQPVQYSQIRVSGPREPAGAPQRHSLSEIT  
YLGQPDISILQPSNVPPPQILSPLSYAPNAAPEVGPPSYAPQVTPEAQFFYAPQAISKVQPSSY  
APQATPDSWPPSYGVCMEGSGKDSPTGTLSSPKHLRPGQLQKEPPAGSCMLGGLSLQEVTSLAM  
EESQEAKSLHQPLGICTDRTSDPNVLHSGEETPQYLKGQLPLLSSVQIEGHPMSLPLQPPSGPC  
SPSDQGPSPWGLLESILVCPKDEAKSPAPETSDLEQPTELDSLFRGLALTQWES

### **Signal sequence.**

amino acids 1-17

### **Transmembrane domain.**

amino acids 233-250

### **N-glycosylation sites.**

amino acids 80-83, 87-90, 172-175

### **N-myristoylation sites.**

amino acids 11-16, 47-52, 102-107, 531-536, 565-570



## FIGURE 165

TGGCCTACTGGAAAAAAAAAAAAAAAAAAAAAGTCACCCGGGCCCCGGGTGGCCACAACATGG  
CTGCGGCGCCGGGGCTGCTCTTCTGGCTGTTTCGTGCTGGGGGCGCTCTGGTGGGTCCCGGGCCAG  
TCGGATCTCAGCCACGGACGGCGTTTTCTCGGACCTCAAAGTGTGCGGGGACGAAGAGTGCAGCAT  
GTTAATGTACCGTGGGAAGCTCTTGAAGACTTCACGGGCCCTGATTGTCGTTTTGTGAATTTTA  
AAAAAGGTGACGATGTATATGTCTACTACAACTGGCAGGGGGATCCCTTGAACCTTTGGGCTGGA  
AGTGTGAACACAGTTTTTGGATATTTTCCAAAAGATTTGATCAAGGTACTTCATAAATACACGGA  
AGAAGAGCTACATATTCAGCAGATGAGACAGACTTTGTCTGCTTTGAAGGAGGAAGAGATGATT  
TTAATAGTTATAATGTAGAAGAGCTTTTAGGATCTTTGGAACTGGAGGACTCTGTACCTGAAGAG  
TCGAAGAAAGCTGAAGAAGTTTCTCAGCACAGAGAGAAATCTCCTGAGGAGTCTCGGGGGCGTGA  
ACTTGACCCTGTGCCTGAGCCCAGGCATTTCAGAGCTGATTTCAGAGGATGGAGAAGGTGCTTTCT  
CAGAGAGCACCGAGGGGCTGCAGGGACAGCCCTCAGCTCAGGAGAGCCACCCTCACACCAGCGGT  
CCTGCGGCTAACGCTCAGGGAGTGCAGTCTTCGTTGGACACTTTTGAAGAAATTCTGCACGATAA  
ATTGAAAGTGCCGGGAAGCGAAAGCAGAACTGGCAATAGTTCTCCTGCCCTCGGTGGAGCGGGAGA  
AGACAGATGCTTACAAAGTCCTGAAAACAGAAATGAGTCAGAGAGGAAGTGGACAGTGCCTTATT  
CATTACAGCAAAGGATTTTCGTTGGCATCAAAATCTAAGTTTGTTTTACAAAGATTGTTTTTAGTA  
CTAAGCTGCCTTGGCAGTTTGCATTTTTGAGCCAAACAAAAATATATTATTTTCCCTTCTAAGTA  
AAAAAAAAAAAAAAAAAAAA

## **FIGURE 166**

MAAAPGLLFWLFWLGALWWVPGQSDLHGRRFSDLKVCGDEECMLMYRGKALEFTGPD CRFVN  
FKKGDDVYVYKLAGGSLELWAGSVEHSFGYFPKDLIKVLHKYTEELHIPAETDFVCFEGGRD  
DFNSYNVEELLGSLELEDSVPEESKKAEEVSQHREKSPEESRGRELDPVPEPEAFRA DSEDGEGA  
FSESTEGLOGQPSAQESHPTSGPAANAQGVQSSLDTFEEILHDKLKVPGSESRTGNSSPASVER  
EKTDAYKVLKTEMSQRGSGQCVIHYSKGFRWHQNL SLFYKDCF

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**N-glycosylation site.**

amino acids 294-298

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-34

**Tyrosine kinase phosphorylation site.**

amino acids 67-76

**N-myristoylation sites.**

amino acids 205-211, 225-231, 277-283

**Amidation site.**

amino acids 28-32

## FIGURE 167

CCAGGACCAGGGCGCACCGGCTCAGCCTCTCACTTGTGAGAGGCCGGGGAAGAGAAGCAAAGCGC  
 AACGGTGTGGTCCAAGCCGGGGCTTCTGCTTCGCTCTAGGACATACACGGGACCCCTAACTTC  
 AGTCCCCCAAACGCGCACCTCGAAGTCTTGAAGTCCAGCCCCGCACATCCACGCGCGGCACAGG  
 CGCGGCAGGCGGCGAGGTCCCGGCCGAAGGCGATGCGCGCAGGGGGTTCGGGCAGCTGGGCTCGGGC  
 GGCGGGAGTAGGGCCCGCAGGAGGCGAGGAGGCTGCATATTCAGAGTCGCGGGCTGCGCCCTG  
 GGCAGAGGCCGCCCTCGCTCCACGCAACACCTGCTGCTGCCACCGCGCGCGATGAGCCGCGTGG  
 TCTCGCTGCTGCTGGGCGCGCGCTGCTCTGCGGCCACGGAGCCTTCTGCCGCGCGTGGTTCAGC  
 GGCCAAAAGGTGTGTTTTGCTGACTTCAAGCATCCCTGCTACAAAATGGCTACTTCCATGAAGT  
 GTCCAGCCGAGTGAGCTTTTCCAGGAGGCACGCTGGCTTGTGAGAGTGAGGGAGGAGTCTCTCA  
 GCCTTGAGAATGAAGCAGAACAGAAGTTAATAGAGAGCATGTTGCAAAACCTGACAAAACCCGGG  
 ACAGGGATTTCTGATGGTGATTTCTGGATAGGGCTTTGGAGGAATGGAGATGGGCAACATCTGG  
 TGCTGCCCAGATCTCTACAGTGGTCTGATGGAAGCAATCCCAGTACCGAACTGGTACACAG  
 ATGAACCTTCCCGGGAAGTGAAAGTGTGTTGTGATGTATCACCACCAACTGCCAATCCTGGC  
 CTTGGGGGTCCCTTACCTTTTACAGTGGATGATGACAGGTGTAACATGAAGCACAATTATATTTG  
 CAAGTATGAACCAGAGATTAATCCAACAGCCCTGTAGAAAAGCCTTATCTTACAAATCAACCAG  
 GAGACCCCATCAGAATGTGGTGTACTGAAGCAGGTATAATTCCCAATCTAATTTATGTTGTT  
 ATACCAACAATACCCTGCTCTTACTGATCTGCTTTTGGAACTGTGTTTCCAGATGCT  
 GCATAAAAGTAAAGGAAGAACAAAAGTGTCCAAACAGTCTACACTGTGGATTTCAAAGAGTA  
 CCAGAAAAGAAAGTGGCATGGAAGTATAAATACTATTGACTTGGTTCCAGAATTTTGAATTTCT  
 GGATCTGTATAAGGAATGGCATCAGAACAATAGCTTGGAATGGCTTGAAATCACAAGGATCTGC  
 AAGATGAAGTGAAGCTCCCCCTTGAGGCAAAATATTAAAGTAATTTTATATGTCTATTATTTC  
 TTTAAAGATATGCTGTGCTAATAATGGAGTGAGACATGCTTATTTTGTAAAGGATGCACCCAA  
 ACTTCAAACCTTCAAGCAAATGAAATGGACAATGCAGATAAAGTTGTTATCAACACGTCGGGAGTA  
 TGTGTGTTAGAAGCAATTCCTTTTATTTCTTTCACCTTTCATAAGTTGTTATCTAGTCAATGTAA  
 TGTATATTGTATTGAAATTTACAGTGTGCAAAAGTATTTTACCTTTGCATAAGTGTGTTGATAAAA  
 ATGAAGTGTCTAATATTTATTTTATGGCATCTCATTTTCAATACATGCTCTTTTGTATTAAG  
 AAACCTTATTACTGTTGTCAACTGAATTCACACACACACAAATATAGTACCATAGAAAAAGTTGT  
 TTTCTCGAAATAATTCATCTTTACGCTTCTCTGCTTTTGGTCAATGTCTAGGAAATCTCTCAGA  
 AATAAGAGCTATTTTATTAAGTGTGATATAAACCTCCTCAAACATTTTACTTAGAGGCAAGGAT  
 TGTCTAATTTCAATTGTGCAAGACATGTGCCTTATAATTATTTTAGCTTAAATTAACAGATT  
 TTGTAATAATGTAACCTTTGTTAATAGGTGCATAAACACTAATGCAGTCAATTTGAACAAAAGAG  
 TGACATACACAATATAAATCATATGTCTTCACACGTTGCCATATAATGAGAAGCAGCTCTCTGA  
 GGGTTCTGAAATCAATGTGGTCCCTCTCTTGCCCACTAAACAAAGATGGTTGTTTCGGGGTTTGGG  
 ATTGACACTGGAGGCAGATAGTTGCAAAGTTAGTCTAAGTTTCCCTAGCTGTATTTAGCCTCTG  
 ACTATATTAGTATACAAAGAGGTCATGTGGTTGAGACCAGGTGAATAGTCACTATCAGTGTGGAG  
 ACAAGCACAGCACACAGACATTTTAGGAAGGAAGGAACACGAAATCGTGTGAAAATGGGTTGG  
 AACCCATCAGTGATCGCATATTCATTGATGAGGGTTTGTCTGAGATAGAAAATGGTGGCTCCTTT  
 CTGTCTTATCTCCTAGTTTCTTCAATGCTTACGCCTTGTCTCTCAAGAGAAAGTTGTAAGTCT  
 CTGGTCTCATATGTCCTGTGCTCCTTTTAAACCAATAAAGAGTTCCTTGTCTTCTGGGGGAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 168**

MSRVVSLLLGAALLCGHGAFCRRVVSQGKVCFADFKHPCYKMAFYHELSSRVSFQEARLACESE  
GGVLLSLENEAEQKLIESMLQNLTKPGTGISDGDGFWIGLWRNGDGQTSGACPDLYQWSDGSNSQ  
YRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWDDRCNMKHNYICKYEPEINPTAPVEK  
PYLTNQPGDTHQNVVVTEAGIIPNLIYVVIPTIPLLLLILVAFGTCCFQMLHKSkgRrTKTSPNQ  
STLWISKSTRKESGMEV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**Transmembrane domain:**

amino acids 214-235

**N-glycosylation sites.**

amino acids 86-89, 255-258

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 266-269

**N-myristoylation sites.**

amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-145, 212-217